

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds  
(without alignments)  
1230.131 Million cell updates/sec

Title: US-10-006-818a-77  
Perfect score: 1816  
Sequence: 1 MALPBRILLWKLVLQSSAV.....SPLPAKYIDLDKGRKCNCK 341

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 19Jun03:\*

|     |   |
|-----|---|
| 1:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.* |
| 2:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.* |
| 3:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.* |
| 4:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.* |
| 5:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.* |
| 6:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.* |
| 7:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.* |
| 8:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.* |
| 9:  | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.* |
| 10: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.* |
| 11: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.* |
| 12: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.* |
| 13: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.* |
| 14: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.* |
| 15: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.* |
| 16: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.* |
| 17: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.* |
| 18: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.* |
| 19: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.* |
| 20: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.* |
| 21: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.* |
| 22: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.* |
| 23: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.* |
| 24: | /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description        |
|------------|--------|-------------|--------|-------|--------------------|
| 1          | 1816   | 100.0       | 341    | 21    | Human PRO1293 prot |
| 2          | 1816   | 100.0       | 341    | 21    | Human PRO1293 (UNQ |
| 3          | 1816   | 100.0       | 341    | 22    | Protein of the inv |
| 4          | 1755.5 | 96.7        | 442    | 22    | Human protein havi |
| 5          | 1755.5 | 96.7        | 442    | 24    | Human SECP-4 prote |
| 6          | 1706   | 93.9        | 384    | 21    | Human MTC48. Homo  |
| 7          | 1694.5 | 93.3        | 450    | 22    | Human protein sequ |
| 8          | 1367.5 | 75.3        | 442    | 23    | Rat protein isolat |
| 9          | 1362.5 | 75.0        | 442    | 22    | Murine adipocytes- |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 1300  | 71.6 | 269 | 22 | ABBI0350 | Human cDNA SEQ ID  |
| 11 | 1300  | 71.6 | 269 | 23 | ABP66937 | Human polypeptide  |
| 12 | 1006  | 55.4 | 290 | 21 | AA859011 | Breast and ovarian |
| 13 | 955   | 52.6 | 192 | 22 | ABBI0523 | Human cDNA SEQ ID  |
| 14 | 955   | 52.6 | 192 | 22 | AAU18028 | Human immunoglobul |
| 15 | 955   | 52.6 | 192 | 23 | ABP67110 | Human polypeptide  |
| 16 | 840   | 45.3 | 255 | 23 | ABP72366 | Murine protein iso |
| 17 | 826.5 | 45.5 | 260 | 21 | AA836108 | Mouse MTC48. Mus   |
| 18 | 355   | 19.5 | 218 | 24 | AB84671  | Human SECP-23 prot |
| 19 | 127   | 7.0  | 447 | 24 | ABR39440 | Human GENSET polyp |
| 20 | 125.5 | 6.9  | 651 | 19 | AAW62782 | Protein encoded by |
| 21 | 125   | 6.9  | 244 | 22 | AA846060 | Human Tf anti-idio |
| 22 | 123   | 6.8  | 550 | 19 | AAW82544 | Human LIR-P3G2 pro |
| 23 | 123   | 6.8  | 650 | 21 | AA804169 | Leukocyte immunogl |
| 24 | 122   | 6.7  | 253 | 23 | ABP45328 | Human Blys binding |
| 25 | 122   | 6.7  | 652 | 19 | AAW82545 | Human LIR-18A3 pro |
| 26 | 122   | 6.7  | 652 | 21 | AA804170 | Leukocyte immunogl |
| 27 | 121   | 6.7  | 254 | 23 | ABP45955 | Human Blys binding |
| 28 | 120   | 6.6  | 266 | 23 | ABG97835 | Single chain antib |
| 29 | 120   | 6.6  | 266 | 23 | ABG35336 | Thrombopoietin ago |
| 30 | 119.5 | 6.6  | 246 | 21 | AAV15126 | Anti-murine CTLA-4 |
| 31 | 119.5 | 6.6  | 249 | 23 | ABP45951 | Human Blys binding |
| 32 | 119   | 6.6  | 240 | 22 | AAW82551 | Human Tf anti-idio |
| 33 | 118.5 | 6.5  | 448 | 19 | AAW82551 | Human LIR-pbm2 pro |
| 34 | 118.5 | 6.5  | 448 | 19 | AAW53463 | Human gp49 HM18 po |
| 35 | 118.5 | 6.5  | 448 | 21 | AA804176 | Leukocyte immunogl |
| 36 | 118.5 | 6.5  | 469 | 22 | AAW41582 | Human polypeptide  |
| 37 | 117.5 | 6.5  | 472 | 19 | AAW69234 | PCR-IV protein seq |
| 38 | 117   | 6.4  | 239 | 22 | AAW46059 | Human Tf anti-idio |
| 39 | 116.5 | 6.4  | 244 | 20 | AAV06718 | Antibody 12E10 sin |
| 40 | 116.5 | 6.4  | 328 | 23 | AAO19049 | Cell adhesion mole |
| 41 | 116   | 6.4  | 253 | 23 | ABP45591 | Human Blys binding |
| 42 | 115.5 | 6.4  | 249 | 23 | ABP45607 | Human Blys binding |
| 43 | 115.5 | 6.4  | 251 | 23 | ABP45535 | Human Blys binding |
| 44 | 115.5 | 6.4  | 533 | 22 | AAW93372 | Human polypeptide, |
| 45 | 115.5 | 6.4  | 534 | 22 | AAU00906 | Human B lymphocyte |

ALIGNMENTS

RESULT 1  
AAB24031  
ID AAB24031 standard; Protein; 341 AA.  
AC AAB24031;  
DT 25-JAN-2001 (first entry)  
XX Human PRO1293 protein sequence SEQ ID NO:31.  
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
KW identification; tumorigenesis; anticancer; detection.  
XX Homo sapiens.  
XX WO2000053750-A1.  
XX 14-SEP-2000  
XX 02-DEC-1999; 99WO-US28551.  
XX 08-MAR-1999; 99WO-US05028.  
XX 01-SEP-1999; 99WO-US20111.  
XX 29-OCT-1999; 99US-0162506.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28634.  
XX (GETH ) GENENTECH INC.  
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
XX WPI; 2000-594320/56.



PR 07-OCT-1998; 98US-0103395.  
PR 07-OCT-1998; 98US-0103396.  
PR 07-OCT-1998; 98US-0103401.  
PR 08-OCT-1998; 98US-0103633.  
PR 08-OCT-1998; 98US-0103678.  
PR 08-OCT-1998; 98US-0103679.  
PR 08-OCT-1998; 98US-0103711.  
PR 14-OCT-1998; 98US-0104257.  
PR 20-OCT-1998; 98US-0104987.  
PR 20-OCT-1998; 98US-0105000.  
PR 20-OCT-1998; 98US-0105002.  
PR 21-OCT-1998; 98US-0105104.  
PR 22-OCT-1998; 98US-0105169.  
PR 22-OCT-1998; 98US-0105266.  
PR 26-OCT-1998; 98US-0105693.  
PR 26-OCT-1998; 98US-0105694.  
PR 26-OCT-1998; 98US-0105807.  
PR 27-OCT-1998; 98US-0105881.  
PR 27-OCT-1998; 98US-0105882.  
PR 27-OCT-1998; 98US-0106062.  
PR 28-OCT-1998; 98US-0106023.  
PR 28-OCT-1998; 98US-0106029.  
PR 28-OCT-1998; 98US-0106030.  
PR 28-OCT-1998; 98US-0106032.  
PR 28-OCT-1998; 98US-0106033.  
PR 28-OCT-1998; 98US-0106178.  
PR 29-OCT-1998; 98US-0106248.  
PR 29-OCT-1998; 98US-0106384.  
PR 29-OCT-1998; 98US-0108500.  
PR 30-OCT-1998; 98US-0106464.  
PR 03-NOV-1998; 98US-0106856.  
PR 03-NOV-1998; 98US-0106902.  
PR 03-NOV-1998; 98US-0106905.  
PR 03-NOV-1998; 98US-0106919.  
PR 03-NOV-1998; 98US-0106932.  
PR 03-NOV-1998; 98US-0106934.  
PR 10-NOV-1998; 98US-0107783.  
PR 17-NOV-1998; 98US-0108775.  
PR 17-NOV-1998; 98US-0108779.  
PR 17-NOV-1998; 98US-0108787.  
PR 17-NOV-1998; 98US-0108788.  
PR 17-NOV-1998; 98US-0108801.  
PR 17-NOV-1998; 98US-0108802.  
PR 17-NOV-1998; 98US-0108806.  
PR 17-NOV-1998; 98US-0108807.  
PR 17-NOV-1998; 98US-0108867.  
PR 17-NOV-1998; 98US-0108925.  
PR 18-NOV-1998; 98US-0108848.  
PR 18-NOV-1998; 98US-0108849.  
PR 18-NOV-1998; 98US-0108850.  
PR 18-NOV-1998; 98US-0108851.  
PR 18-NOV-1998; 98US-0108852.  
PR 18-NOV-1998; 98US-0108858.  
PR 18-NOV-1998; 98US-0108904.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
XX  
XX WPI; 2000-237871/20.  
DR N-PSDB; AAA37044.  
XX  
XX New mammalian DNA sequences encoding transmembrane, receptor or  
PT secreted PRO polypeptides, useful for screening of potential peptide or  
PT small molecule inhibitors of the relevant receptor/ligand interactions  
PT  
XX  
XX Claim 12; Fig 46; 773pp; English.  
XX  
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences

CC encoding then have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent  
CC PCR primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention.  
XX  
SQ Sequence 341 AA;  
Query Match 100.0%; Score 1816; DB 21; Length 341;  
Best Local Similarity 100.0%; Pred. No. 4.8e-155;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPP 60  
|||  
DB 1 MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPP 60  
|||  
QY 61 ATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADR 120  
|||  
DB 61 ATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADR 120  
|||  
QY 121 LLDLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHHYCGL 180  
|||  
DB 121 LLDLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHHYCGL 180  
|||  
QY 181 HERRVEHLTVAEPHAEPGRGSPONGSSHSAGPPDPTLARGHNVINIVPESRAHFFQ 240  
|||  
DB 181 HERRVEHLTVAEPHAEPGRGSPONGSSHSAGPPDPTLARGHNVINIVPESRAHFFQ 240  
|||  
QY 241 LGYVLATLLLFILLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEPFAVAGDQMLYR 300  
|||  
DB 241 LGYVLATLLLFILLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEPFAVAGDQMLYR 300  
|||  
QY 301 SEDIQLDYKNNILKERABLAHSPAPKYIDLKGFRENCK 341  
|||  
DB 301 SEDIQLDYKNNILKERABLAHSPAPKYIDLKGFRENCK 341  
|||  
RESULT 3  
AAB66111  
ID AAB66111 standard; protein; 341 AA.  
XX  
AC AAB66111;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Protein of the invention #23.  
XX  
KW Secreted; transmembrane; gene therapy.  
XX  
OS Unidentified.  
XX  
PN WO200078961-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 18-FEB-2000; 2000WO-US04342.  
XX  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 16-DEC-1999; 99WO-US30095.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
PI Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-071395/08.  
 DR Secreted and transmembrane proteins and nucleic acids designated PRO,  
 XX useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy -  
 PT  
 XX  
 PS Claim 1; Fig 46; 787pp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of  
 CC anti-sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents.  
 CC The nucleic acids may also be used in gene therapy.  
 XX  
 SQ Sequence 341 AA;  
 Query Match 100.0%; Score 1816; DB 22; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-155;  
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALPSRILLKLLVLLQSSAVLLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPP 60  
 Db 1 MALPSRILLKLLVLLQSSAVLLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPP 60  
 QY 61 ATPAYWGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDROPVPHDRADR 120  
 Db 61 ATPAYWGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDROPVPHDRADR 120  
 QY 121 LLDLYASGERRAYGFLFDRVAVGADAFERDPSLRLEPLEVADGTYSCHLHHYCG 180  
 Db 121 LLDLYASGERRAYGFLFDRVAVGADAFERDPSLRLEPLEVADGTYSCHLHHYCG 180  
 QY 181 HRRVPHLTVAEPHAEPPRSGSSHSGAPGDPPTLARGHNVINIVPESRAHFQQ 240  
 Db 181 HRRVPHLTVAEPHAEPPRSGSSHSGAPGDPPTLARGHNVINIVPESRAHFQQ 240  
 QY 241 LGYVLATLLLFILLVTVLLAARRRGVEYSDQSGKSKGVNLAFAVAAGDQMLYR 300  
 Db 241 LGYVLATLLLFILLVTVLLAARRRGVEYSDQSGKSKGVNLAFAVAAGDQMLYR 300  
 QY 301 SEDIQDYKXNLLKERAELAHSLPAPKATIDLDKGRKENCK 341  
 Db 301 SEDIQDYKXNLLKERAELAHSLPAPKATIDLDKGRKENCK 341  
 RESULT 4  
 AAE06578 standard; Protein; 442 AA.  
 XX  
 AC AAE06578;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human protein having hydrophobic domain, HP10769.  
 XX  
 KW Human; hydrophobic domain; gene therapy; nutritional supplement;  
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;  
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;  
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;  
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;  
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;  
 KW contraceptive; antiinfertility; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200149728-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-JP09359.

XX 06-JAN-2000; 2000JP-0000585.  
 PR 06-JAN-2000; 2000JP-0000588.  
 PR 11-JAN-2000; 2000JP-0002299.  
 PR 03-FEB-2000; 2000JP-0026862.  
 PR 03-MAR-2000; 2000JP-0058367.  
 XX  
 PA (PROT-) PROTEGENE INC.  
 PA (SAGA) SAGAMI CHEM RES CENT.  
 XX  
 Kato S, Kimura T;  
 WPI; 2001-418355/44.  
 DR N-PSDB; AAD12573.  
 XX  
 PT Human proteins with hydrophobic domains and the nucleic acids encoding  
 PT them, useful for preventing diagnosing and treating e.g. cancer,  
 PT Alzheimer's and inflammation -  
 PT  
 XX  
 PS Claim 1; Page 236-238; 563pp; English.  
 XX  
 CC The present sequence is human protein with hydrophobic domain,  
 CC HP10769. The polynucleotide and polypeptide of the invention  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The polynucleotides  
 CC may be used to produce the polypeptide, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. The  
 CC polynucleotides and its complementary sequences may also be used as DNA  
 CC probes in diagnostic assays and also used in gene therapy. The  
 CC polypeptides may also be used as antigens in the production of antibodies  
 CC and in assays to identify modulators of polypeptide expression and  
 CC activity. The polypeptides and nucleic acids may be used as nutritional  
 CC supplements, to modulate cytokine and cell proliferation activity, to  
 CC modulate immune stimulation or suppression (e.g. for the treatment of  
 CC microbial infections and autoimmune disorders such as multiple sclerosis,  
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate  
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the  
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's  
 CC disease), to modulate activin and inhibin activity (e.g. for controlling  
 CC fertility), to modulate chemotactic and chemokinetic activity, to  
 CC modulate haemostatic and thrombolytic activity, to modulate receptor  
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.  
 XX  
 SQ Sequence 442 AA;  
 Query Match 96.7%; Score 1755.5; DB 22; Length 442;  
 Best Local Similarity 77.1%; Pred. No. 1.8e-149;  
 Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;  
 QY 1 MALPSRILLKLLVLLQSSAVLLHLS----- 24  
 Db 1 MALPSRILLKLLVLLQSSAVLLHSGSSVPAAGSSVVSSEAVSWEAGARAVLRQSPRMV 60  
 QY 25 ----- 24  
 Db 61 WTQDRHLHQRVRLHWDLRGPGGGPARRLLDLYSAGFQVYEARDGRLELSASAFDDGNF 120  
 QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 79  
 Db 121 SLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 180  
 QY 80 PALLTCVNRGHVWTDHVEEAQQVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 139  
 Db 181 PALLTCVNRGHVWTDHVEEAQQVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 240  
 QY 140 DRVAVGADAFERDPSLRLEPLEVADGTYSCHLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 199  
 Db 241 DRVAVGADAFERDPSLRLEPLEVADGTYSCHLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 300  
 QY 200 RGSPGNSSSHSGAPGDPPTLARGHNVINIVPESRAHFQQLGYVLATLLLFILLVTVL 259  
 Db 301 RGSPGNSSSHSGAPGDPPTLARGHNVINIVPESRAHFQQLGYVLATLLLFILLVTVL 360



QY 260 LAARRRRGGYEYSDQSGKSGKDVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAEL 319  
DB 361 LAARRRRGGYEYSDQSGKSGKDVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAEL 420  
QY 320 AHSPLPAKYIDLKGFRENCK 341  
DB 421 AHSPLPAKYIDLKGFRENCK 442

RESULT 5  
ID ABB84652  
XX ABB84652 standard; Protein; 442 AA.  
AC ABB84652;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Human SECP-4 protein from clone 1345785CD1 SEQ ID 4.  
XX  
KW Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;  
KW hepatotropic; cytostatic; anti-HIV; anti-allergic; antiasthmatic; cancer;  
KW antianaemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer;  
KW antirheumatic; antiarthritic; cardiac; hypotensive; gonadal dysgenesis;  
KW vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis;  
KW antiparkinsonian; ophthalmological; cell proliferative disorder;  
KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris;  
KW autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy;  
KW ulcerative colitis; cardiovascular disorder; myocardial infarction;  
KW Raynaud's disease; myocardiitis; neurological disorder; cataract;  
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;  
KW developmental disorder; Duchenne muscular dystrophy; antipsoriatic;  
KW Becker muscular dystrophy; Cushing's syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200279441-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-US09920.  
XX  
PR 30-MAR-2001; 2001US-280527P.  
PR 06-APR-2001; 2001US-282112P.  
PR 09-APR-2001; 2001US-282702P.  
PR 13-APR-2001; 2001US-283855P.  
PR 19-OCT-2001; 2001US-343718P.  
PR 07-DEC-2001; 2001US-339236P.  
PR 13-FEB-2002; 2002US-357002P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe IJ;  
PI Gandhi AR, Gietzen KJ, Griffin JA, He A, Honchell CD, Ison CH;  
PI Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM;  
PI Swarnakar A, Ramkumar J, Tang YT, Thangavelu K, Tran UK, Wallia NK;  
PI Warren BA, Yao MG, Xu Y, Yue H;  
XX  
DR WPI; 2003-058429/05.  
DR N-PSDB; ABB57548.  
XX  
PT Novel human secreted protein useful for treating, preventing or  
PT diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus,  
PT anemia, epilepsy, cataract, Alzheimer's disease  
XX  
PS Claim 59; Page 152-153; 188pp; English.  
XX  
CC This invention describes novel secreted proteins (SECP) which have  
CC antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic,  
CC anti-HIV, anti-allergic, antiasthmatic, antianaemic, antidiabetic,  
CC antiinflammatory, neuroprotective, antiulcer, antipsoriatic, vasotropic,  
CC antirheumatic, antiarthritic, cardiac, hypotensive, anticonvulsant,  
CC nootropic, immunosuppressive, antiparkinsonian and ophthalmological  
CC activity. The polynucleotides and polypeptides of the invention can be

CC used for diagnosing, treating or preventing cell proliferative disorder  
CC e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer,  
CC autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome  
CC (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,  
CC etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,  
CC hypertension, Raynaud's disease, myocardiitis, pericarditis, etc;  
CC neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's  
CC disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and  
CC developmental disorders e.g. Duchenne and Becker muscular dystrophy,  
CC cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of  
CC the invention can also be used for drug screening, proteome analysis,  
CC microarrays creating knock-in humanised animals or transgenic animals to  
CC model human diseases, in somatic or germline gene therapy, to generate a  
CC transcript image of a tissue or cell type, for detecting differences in  
CC the chromosomal location due to translocation, inversion, etc., among  
CC normal, carrier or affected individuals, and as hybridization probes for  
CC mapping naturally occurring genomic sequences. ABB84649-ABB84673  
CC represent secreted proteins encoded by the cDNA's shown in  
CC ABB57545-ABB57569, described in the disclosure of the invention.

XX SQ Sequence 442 AA;  
Query Match 96.7%; Score 1755.5; DB 24; Length 442;  
Best Local Similarity 77.1%; Pred. No. 1.8e-149;  
Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;  
QY 1 MALPSRILLWKLVLQSSAVLLHS----- 24  
DB 1 MALPSRILLWKLVLQSSAVLLHS----- 60  
QY 25 ----- 24  
DB 61 WTQDLHQRVLRVHDLRGPGGPARLLDLYSAGEQRYVEARDGRLELSAFAFDGDNF 120  
QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 79  
DB 121 SLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKVLAVARGA 180  
QY 80 PALLTCVNRGHVWTDHRHVEAQVHVWDRQPGVPHDRADRLDLVSGERRAYGPLEFLR 139  
DB 181 PALLTCVNRGHVWTDHRHVEAQVHVWDRQPGVPHDRADRLDLVSGERRAYGPLEFLR 240  
QY 140 DRVAVGADAFERGFSLRIEPLVLEVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEP 199  
DB 241 DRVAVGADAFERGFSLRIEPLVLEVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEP 300  
QY 200 RGSPGNGSSHSGAGPDPPTLARGHNVINVIPESSRAHFFQQLGYVLATLLFILLVTVL 259  
DB 301 RGSPGNGSSHSGAGPDPPTLARGHNVINVIPESSRAHFFQQLGYVLATLLFILLVTVL 360  
QY 260 LAARRRRGGYEYSDQSGKSGKDVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAEL 319  
DB 361 LAARRRRGGYEYSDQSGKSGKDVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAEL 420  
QY 320 AHSPLPAKYIDLKGFRENCK 341  
DB 421 AHSPLPAKYIDLKGFRENCK 442

RESULT 6  
ID AAB36107  
XX AAB36107 standard; Protein; 384 AA.  
XX  
AC AAB36107;  
XX  
DT 20-FEB-2001 (first entry)  
XX  
DE Human MTC48.  
XX  
KW Human; cytostatic; metastatic thyroid cancer; MTC; thyroid carcinoma.  
XX  
OS Homo sapiens.

XX WO200063438-A2.  
XX 26-OCT-2000.  
XX 20-APR-2000; 2000WO-US10729.  
XX 20-APR-1999; 99US-0130123.  
XX 30-MAR-2000; 2000US-0193203.  
XX 19-APR-2000; 2000US-0552322.  
XX (CURA-) CURAGEN CORP.  
XX Gould-Rothberg BE, Rastelli L;  
XX WPI; 2000-665252/64.  
XX N-PSDB; AAC67985.  
XX Categorizing, diagnosing or assessing the prognosis of thyroid  
XX carcinoma by measuring the expression levels of MTC (metastatic thyroid  
XX cancer) genes -  
XX Disclosure; Page 33; 105pp; English.  
XX The present sequence is a novel metastatic thyroid cancer (MTC)  
XX protein. A method of categorizing, diagnosing or assessing the prognosis  
XX of thyroid carcinoma by measuring the expression levels of MTC genes is  
XX disclosed. The MTC genes are differentially expressed in metastatic  
XX thyroid cancer when compared to non-metastatic thyroid cancer. An  
XX agent that decreases the expression or activity of one or more MTC genes  
XX may be administered to treat metastatic carcinoma. Allele-specific  
XX oligonucleotide probes that hybridize to an MTC polynucleotide at a  
XX polymorphic site may be used to determine whether a subject suffers from  
XX or is at risk of metastatic thyroid carcinoma.  
XX Sequence 384 AA;  
XX Query Match 93.9%; Score 1706; DB 21; Length 384;  
XX Best Local Similarity 99.4%; Pred. No. 4.4e-145;  
XX Matches 319; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 80  
Db 64 LLRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 123  
QY 81 ALLTCVNRGHVWTDHRVVEAQVWVHWRQPPGVPHDRADRLDLYASGERRAYGPLEFLRD 140  
Db 124 ALLTCVNRGHVWTDHRVVEAQVWVHWRQPPGVPHDRADRLDLYASGERRAYGPLEFLRD 183  
QY 141 RVAVGADAFERGFSLRIEPLVLEVADEGTYSCHLHHYCHLHERRVFLHTVAEPHAEPPPPR 200  
Db 184 RVAVGADAFERGFSLRIEPLVLEVADEGTYSCHLHHYCHLHERRVFLHTVAEPHAEPPPPR 243  
QY 201 GSPGNGSSHGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLATLLFILLVTVLL 260  
Db 244 GSPGNGSSHGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLATLLFILLVTVLL 303  
QY 261 AARRRGGEYSDQSKSGKGVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAELA 320  
Db 304 AARRRGGEYSDQSKSGKGVNLAFAVAAGDQMLYRSEDIQLDYKNNILKERAELA 363  
QY 321 HSPLPAKYIIDLDKGFRENCK 341  
Db 364 HSPLPAKYIIDLDKGFRENCK 384  
RESULT 7  
ID AAB92464  
XX AAB92464 standard; Protein; 450 AA.  
XX AC AAB92464;  
XX DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:10520.  
XX DE  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX KW  
XX Homo sapiens.  
XX OS  
XX EP1074617-A2.  
XX PN  
XX 07-FEB-2001.  
XX PD  
XX 28-JUL-2000; 2000EP-0116126.  
XX PF  
XX 29-JUL-1999; 99JP-0248036.  
XX PR 27-AUG-1999; 99JP-0300253.  
XX PR 11-JAN-2000; 2000JP-0118776.  
XX PR 02-MAY-2000; 2000JP-0183767.  
XX PR 09-JUN-2000; 2000JP-0241899.  
XX (HELI-) HELIX RES INST.  
XX PA  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX DR  
XX Primer sets for synthesizing polynucleotides, particularly the 5602  
XX full-length cDNAs defined in the specification, and for the detection  
XX and/or diagnosis of the abnormality of the proteins encoded by the  
XX full-length cDNAs -  
XX Claim 8; SEQ ID 10520; 2537pp + CD ROM; English.  
XX The present invention describes primer sets for synthesizing 5602  
XX full-length cDNAs defined in the specification. Where a primer set  
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
XX to the complementary strand of a polynucleotide which comprises one of  
XX the 5602 nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
XX of an oligonucleotide comprising a sequence complementary to the  
XX complementary strand of a polynucleotide which comprises a 5'-end  
XX sequence and an oligonucleotide comprising a sequence complementary to a  
XX polynucleotide which comprises a 3'-end sequence, where the  
XX oligonucleotide comprises at least 15 nucleotides and the combination of  
XX the 5'-end sequence/3'-end sequence is selected from those defined in  
XX the specification. The primer sets can be used in antisense therapy and  
XX in gene therapy. The primers are useful for synthesizing polynucleotides,  
XX particularly full-length cDNAs. The primers are also useful for the  
XX detection and/or diagnosis of the abnormality of the proteins encoded by  
XX the full-length cDNAs. The primers allow obtaining of the full-length  
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
XX represent oligonucleotides, all of which are used in the exemplification  
XX of the present invention.

XX SQ Sequence 450 AA;

Query Match 93.3%; Score 1694.5; DB 22; Length 450;  
Best Local Similarity 75.5%; Pred. No. 5.8e-144;  
Matches 332; Conservative 1; Mismatches 0; Indels 107; Gaps 2;

QY 1 MALPSRILLWKLVLLQSSAVLLHS----- 24  
Db 1 MALPSRILLWKLVLLQSSAVLLHS----- 60  
QY 25 ----- 24  
Db 61 WTQDRILHQRVRLHWDLRPGGPPARRLLDLYSAGEQRVYEARDRGRLSASAFDDGNF 120  
QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 79  
Db 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 180

QY 80 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLLDLYASGERRAYGPFLELR 139  
DB 181 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLLDLYASGERRAYGPFLELR 240  
QY 140 DRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVHFLTVAEPAEPPPP 199  
DB 241 DRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVHFLTVAEPAEPPPP 300  
QY 200 RGSFGNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQOLGYVATLILLVTVL 259  
DB 301 RGSFGNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQOLGYVATLILLVTVL 360  
QY 260 LAARRRRGGYEYSQKSGKGDVNLAEFAVAAGDQMLYRSEDIDL-----DYKNNIL 313  
DB 361 LAARRRRGGYEYSQKSGKGDVNLAEFAVAAGDQMLYRSEDVQLASSPPTDYKNNIL 420  
QY 314 KERAELAHSPILPAKYIDLDK 333  
DB 421 KERAELAHSPILPAKYIDLDK 440

RESULT 8  
ABB72335

ID ABB72335 standard; Protein; 442 AA.

XX ABB72335;

DT 04-APR-2002 (first entry)

XX Rat protein isolated from skin cells SEQ ID NO: 659.

DE Human; rat; mouse; skin cell; skin wound; cancer; growth defect;  
KW developmental defect; inflammatory disease; dermatological; vulnary;  
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

XX Rattus sp.

XX WO200190357-A1.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-NZ00099.

XX 24-MAY-2000; 2000US-206650P.

XX 25-JUL-2000; 2000US-221232P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble XD;

XX WPI; 2002-122020/16.

XX N-PSDB; ABL35021.

XX New polynucleotides and polypeptides encoded by the polynucleotides  
PT isolated from skin cells, useful for treating skin wounds, cancers,  
PT growth and developmental defects, inflammatory diseases, or for  
PT modulating immune responses

XX Claim 4; Page 416-417; 466pp; English.

XX The present invention provides the protein and coding sequences of cDNAs  
CC isolated from human, murine and rat skin cell libraries. The sequences  
CC can be used in the development of therapeutic agents useful in the  
CC treatment of skin diseases, including skin wounds, cancer, growth  
CC defects, developmental defects and inflammatory diseases. The proteins  
CC have important roles in the induction of hair growth, cell proliferation  
CC and cell-cell interaction, in maintaining tissue integrity, in wound  
CC healing and in modulating immune responses. The present sequence is a  
CC polypeptide of the invention.

XX Sequence 442 AA;

Query Match 75.3%; Score 1367.5; DB 23; Length 442;  
Best Local Similarity 61.3%; Pred. No. 1.5e-114;  
Matches 271; Conservative 22; Mismatches 48; Indels 101; Gaps 3;  
QY 1 MALPSRILLWKVLQSSAVL----- 21  
DB 1 MELLRSVLLWKVLQSSAVLSSGSPGTAASSSVVSESAVSWAAGTQAVLRCQSPRMVW 60  
QY 22 ----LHS----- 24  
DB 61 TQDRLEHDRQRVHVWDLGGPGSGRRRLVDMYSAGEQRYVQPRDRRLLLSPSAFHDGNS 120  
QY 25 ----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTDPPTPAYWDGEKEVLAVARGAP 80  
DB 121 LLIRAVERGDEGYTCNLHHYCHLYESLAVRLEVTDDPLLSRAYWDGEKEVLVALGAP 180  
QY 81 ALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLLDLYASGERRAYGPFLELR 140  
DB 181 ALMTCVNRHLEWTDHLEEAQQVHVWDRQPPGVPHDRADRLLDLYASGERRAYGPFLELR 240  
QY 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVHFLTVAEPAEPPPP 200  
DB 241 RVSNTNFAFARGDFSLRIDDLPEADEGIYCHLHHYCGLHERRVHFLTVAEPAEPPPP 300  
QY 201 GSPGNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQOLGYVATLILLVTVL 260  
DB 301 ASPGNGSGHNSVSPDPTMARGHSIINVIVPEDHTHFFQOLGYVATLILLVTVL 360  
QY 261 AARRRR-GGYEYSQKSGKGDVNLAEFAVAAGDQMLYRSEDIDLQDYKNNILKERAEL 319  
DB 361 ATRHSHGGCKTSDRKAGSKGDVNMMEFAIATEDQAPYRTEDIQDYKNNILKERAEL 420  
QY 320 AHSPLPAKYIDLKGRKENCK 341  
DB 421 AHSPLPAKQVDLDKEPRKEYCK 442

RESULT 9

AAB85860

ID AAB85860 standard; Protein; 442 AA.

XX AAB85860;

DT 30-NOV-2001 (first entry)

XX Murine adipocytes-derived protein.

DE Adipocyte; murine; differentiation; obesity; hyperlipemia; diabetes;  
KW atherosclerosis.

XX Mus musculus.

XX WO200165720-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP01863.

XX 10-MAR-2000; 2000JP-0072502.

XX (KITA/) KITAMURA T.

XX (TSUR/) TSURUGA H.

XX Kitamura T, Tsuruga H;

XX WPI; 2001-565585/63.

XX N-PSDB; AAH76374.

XX Genes associated with adipocyte differentiation for screening  
PT adipocyte-related disorders such as diabetes and hyperlipemia

XX Claim 1; Page 85-88; 112pp; Japanese.

XX

CC The invention relates to genes derived from murine adipocytes and  
CC proteins encoded by these genes. The proteins are associated with  
CC adipocyte differentiation and can be expressed by standard recombinant  
CC methodology. The genes, proteins and specific antibodies are useful for  
CC the identification of drugs for treatment and prevention of adipocyte-  
CC related disorders such as obesity, hyperlipemia, diabetes and  
CC atherosclerosis. The present sequence represents a protein encoded by  
CC the gene derived from murine adipocytes.

SQ Sequence 442 AA;

Query Match 75.0%; Score 1362.5; DB 22; Length 442;  
Best Local Similarity 61.3%; Pred. No. 4.3e-114;  
Matches 271; Conservative 21; Mismatches 49; Indels 101; Gaps 3;

Qy 1 MALPSRILLWKLVLLOSSAVL----- 21  
Db 1 MELLGRVLLWKLVLLOSSAVLSGGPGSTAAASNSLVSVSLAAGTQAVLRCCSPRMVW 60  
Qy 22 ----LHS----- 24  
Db 61 TQDRLEHRQVRVHWDLSGGPGSQRRRLVDMYSAGEQVRVYPRDRDRLLLSFSAFHDGNS 120  
Qy 25 ----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEXEVLAVARGAP 80  
Db 121 LLIRAVERGDEGVTCNLHHYCHLDESILVRLVETEDPLLSRAYWDGEXEVLVAHARGAP 180  
Qy 81 ALLTCVNRGHVWTDHVEEAQVQVHWDROPVPHDRDLDDLYASGERRAYGPIFLRD 140  
Db 181 ALMTCTINRAHVWTDHLEEAQVQVHWDROPVSHDRDLDDLYASGERRAYGPPFLRD 240  
Qy 141 RVAGCADAFFERGFDFSLRIEPLVADGTYSCHLHHYCHLHRRVFLHTVAEPHAPPPR 200  
Db 241 RVSNTNFAFGDFSLRIEPLVADGTYSCHLHHYCHLHRRVFLHTVAEPHAPPPR 300  
Qy 201 GSPNGSGSHGAPGPDPTLARGHNVIVPESRAHFFQOLGYVLATLLIFLLVTVLL 260  
Db 301 ASPNGSGSHGAPGPDPTLARGHNVIVPESRAHFFQOLGYVLATLLIFLLVTVLL 360  
Qy 261 AARRRR-GGYEYSDQSGKSGKGVNLAFAVAAGDQMLYRSEDIQLDYKNILKRAEL 319  
Db 361 ATRHRRSGGCKTSDKAGSKGKGVNVMVEFAVATRDQAPYRTEDIQLDYKNILKRAEL 420  
Qy 320 AHSPLPAKYIDLDKGRKENCK 341  
Db 421 AHSPLPAKYIDLDKGRKENCK 442

RESULT 10  
ABB10350  
ID ABB10350 standard; Protein; 269 AA.  
XX  
AC ABB10350;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Human cDNA SEQ ID NO: 658.  
XX  
KW Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation.  
OS Homo sapiens.  
XX  
FN WO200154474-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01349.  
XX  
PR 31-JAN-2000; 2000US-179065P.  
PR 04-FEB-2000; 2000US-180628P.

PR 24-FEB-2000; 2000US-184664P.  
PR 02-MAR-2000; 2000US-186350P.  
PR 16-MAR-2000; 2000US-189874P.  
PR 17-MAR-2000; 2000US-190076P.  
PR 18-APR-2000; 2000US-198123P.  
PR 19-MAY-2000; 2000US-205515P.  
PR 07-JUN-2000; 2000US-209467P.  
PR 28-JUN-2000; 2000US-214886P.  
PR 30-JUN-2000; 2000US-215135P.  
PR 07-JUL-2000; 2000US-216647P.  
PR 07-JUL-2000; 2000US-216880P.  
PR 11-JUL-2000; 2000US-217487P.  
PR 11-JUL-2000; 2000US-217496P.  
PR 14-JUL-2000; 2000US-218290P.  
PR 26-JUL-2000; 2000US-220963P.  
PR 26-JUL-2000; 2000US-220964P.  
PR 14-AUG-2000; 2000US-224518P.  
PR 14-AUG-2000; 2000US-224519P.  
PR 14-AUG-2000; 2000US-225213P.  
PR 14-AUG-2000; 2000US-225214P.  
PR 14-AUG-2000; 2000US-225266P.  
PR 14-AUG-2000; 2000US-225267P.  
PR 14-AUG-2000; 2000US-225268P.  
PR 14-AUG-2000; 2000US-225270P.  
PR 14-AUG-2000; 2000US-225447P.  
PR 14-AUG-2000; 2000US-225757P.  
PR 14-AUG-2000; 2000US-225758P.  
PR 14-AUG-2000; 2000US-225759P.  
PR 18-AUG-2000; 2000US-226279P.  
PR 22-AUG-2000; 2000US-226681P.  
PR 22-AUG-2000; 2000US-226688P.  
PR 22-AUG-2000; 2000US-227182P.  
PR 23-AUG-2000; 2000US-227009P.  
PR 30-AUG-2000; 2000US-228924P.  
PR 01-SEP-2000; 2000US-229287P.  
PR 01-SEP-2000; 2000US-229343P.  
PR 01-SEP-2000; 2000US-229344P.  
PR 01-SEP-2000; 2000US-229345P.  
PR 05-SEP-2000; 2000US-229509P.  
PR 05-SEP-2000; 2000US-229513P.  
PR 06-SEP-2000; 2000US-230437P.  
PR 06-SEP-2000; 2000US-230438P.  
PR 08-SEP-2000; 2000US-231242P.  
PR 08-SEP-2000; 2000US-231243P.  
PR 08-SEP-2000; 2000US-231244P.  
PR 08-SEP-2000; 2000US-231413P.  
PR 08-SEP-2000; 2000US-231414P.  
PR 08-SEP-2000; 2000US-232080P.  
PR 08-SEP-2000; 2000US-232081P.  
PR 12-SEP-2000; 2000US-231968P.  
PR 14-SEP-2000; 2000US-232397P.  
PR 14-SEP-2000; 2000US-232398P.  
PR 14-SEP-2000; 2000US-232399P.  
PR 14-SEP-2000; 2000US-232400P.  
PR 14-SEP-2000; 2000US-232401P.  
PR 14-SEP-2000; 2000US-233063P.  
PR 14-SEP-2000; 2000US-233064P.  
PR 14-SEP-2000; 2000US-233065P.  
PR 21-SEP-2000; 2000US-234223P.  
PR 21-SEP-2000; 2000US-234274P.  
PR 25-SEP-2000; 2000US-234997P.  
PR 25-SEP-2000; 2000US-234998P.  
PR 26-SEP-2000; 2000US-235484P.  
PR 27-SEP-2000; 2000US-235834P.  
PR 27-SEP-2000; 2000US-235836P.  
PR 29-SEP-2000; 2000US-236327P.  
PR 29-SEP-2000; 2000US-236367P.  
PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-236802P.  
PR 02-OCT-2000; 2000US-237037P.  
PR 02-OCT-2000; 2000US-237038P.



PR 14-AUG-2000; 2000US-225267P.  
PR 14-AUG-2000; 2000US-225268P.  
PR 14-AUG-2000; 2000US-225270P.  
PR 14-AUG-2000; 2000US-225447P.  
PR 14-AUG-2000; 2000US-225757P.  
PR 14-AUG-2000; 2000US-225758P.  
PR 22-AUG-2000; 2000US-226868P.  
PR 30-AUG-2000; 2000US-228924P.  
PR 01-SEP-2000; 2000US-229287P.  
PR 01-SEP-2000; 2000US-229343P.  
PR 01-SEP-2000; 2000US-229344P.  
PR 01-SEP-2000; 2000US-229345P.  
PR 05-SEP-2000; 2000US-229509P.  
PR 05-SEP-2000; 2000US-229513P.  
PR 08-SEP-2000; 2000US-231413P.  
PR 21-SEP-2000; 2000US-234223P.  
PR 21-SEP-2000; 2000US-234274P.  
PR 25-SEP-2000; 2000US-234977P.  
PR 27-SEP-2000; 2000US-235834P.  
PR 29-SEP-2000; 2000US-236327P.  
PR 29-SEP-2000; 2000US-236367P.  
PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-236802P.  
PR 02-OCT-2000; 2000US-237037P.  
PR 02-OCT-2000; 2000US-237038P.  
PR 02-OCT-2000; 2000US-237039P.  
PR 02-OCT-2000; 2000US-237040P.  
PR 13-OCT-2000; 2000US-239935P.  
PR 20-OCT-2000; 2000US-240960P.  
PR 20-OCT-2000; 2000US-241785P.  
PR 20-OCT-2000; 2000US-241809P.  
PR 01-NOV-2000; 2000US-244617P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
XX  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
DR WPI; 2002-681727/73.  
DR N-PSDB; ABV83909.  
XX  
PT Novel polypeptide useful for diagnosis, prognosis, prevention, and  
PT treatment of immune, hyperproliferative, renal, respiratory,  
PT cardiovascular, reproductive, endocrine, gastrointestinal and  
PT neurological disorders -  
XX  
PS Claim 11; SEQ ID NO 658; 369pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (ABV83682-ABV84101) and proteins  
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 269 AA;  
Query Match 71.6%; Score 1300; DB 23; Length 269;  
Best Local Similarity 98.4%; Pred. NO. 9.8e-109;  
Matches 239; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 40 HHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTRHVEE 99  
DB 4 HHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTRHVEE 63  
QY 100 AQOVVHWDROPVPHDRADRLLDLYASGERRAYGPIFLDRVAVGADAFERGFSLRIE 159  
DB 64 AQOVVHWDROPVPHDRADRLLDLYASGERRAYGPIFLDRVAVGADAFERGFSLRIE 123  
QY 160 PLEVADEGTYSCHLHHYHCLHERRVFLTVAPHAEPGRGSPGNGSSHSGAPGDPPTL 219  
DB 124 PLEVADEGTYSCHLHHYHCLHERRVFLTVAPHAEPGRGSPGNGSSHSGAPGDPPTL 183  
QY 220 ARGHNVINIVIPESRAHFFQOLGYVLATLLFILLVTVLLAARRRRGGYEYSDQKSGKS 279  
DB 184 ARGHNVINIVIPESRAHFFQOLGYVLATLLFILLVTVLLAARRRRGGYEYSDQKSGSQ 243  
QY 280 KGK 282  
DB 244 RGR 246  
RESULT 12  
AAB59011  
ID AAB59011 standard; Protein; 290 AA.  
XX  
AC AAB59011;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 719.  
XX  
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
KW neutropenic; neutrophilic; antiviral; antiallergic; hepatotropic;  
KW antidiabetic; antiinflammatory; antitumor; antitumor; anticonvulsant;  
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KW cardiovascular disorder; wound healing; neurological disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200055173-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US05881.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-611515/58.  
DR N-PSDB; AAF21914.  
XX  
PT New human breast and ovarian cancer associated gene sequences and the  
PT polypeptides encoded by these genes, useful in the prevention,  
PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
PT disorders and neurological diseases -  
XX  
PS Claim 11; Page 1173-1174; 1299pp; English.  
XX  
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are



CC associated with breast and ovarian cancer. Included in the invention are  
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
CC isolation and characterization of the DNA and protein sequences of the  
CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
CC neutropenic; neuroprotective; antiviral; antiallergic; hepatotropic;  
CC antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;  
CC antibacterial; antifungal; antiparasitic and cardiant activity. The  
CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
CC particularly breast and ovarian cancer. The nucleic acid sequences,  
CC proteins, agonists and antagonists may also be used in the diagnosis,  
CC prevention and treatment of immune disorders e.g. Addison's disease,  
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
CC arthritis and ulcerative colitis; cardiovascular disorders such as  
CC myocardial ischaemia; wound healing; neurological diseases such as  
CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 290 AA;

Query Match 55.4%; Score 1006; DB 21; Length 290;  
Best Local Similarity 64.6%; Pred. No. 3.1e-82;  
Matches 210; Conservative 8; Mismatches 55; Indels 52; Gaps 5;

QY 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYDGEKEVLAVARGAP 80  
Db 14 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYDGEKEVLAVARGAP 72  
QY 81 ALLTCVNRGHVWTDHVEEAQVQVHWDROPVGVPHDRADRLDLYASGERRAYGFLFLRD 140  
Db 73 AXLTICVNRGHVWTDHVEEAQVQVHWDROPVGVPHDRADRLDLYASASALRAP-FAAX 131  
QY 141 RVAVGADAFERGDSEFSLRIEPLVADGTYSCHLHHYCGHLHRRVFLTVAEHPAEP 200  
Db 132 RVAVGADAFERGDSEFSLRIEPLVADGTYSCHLHHY----- 168  
QY 201 GSPGNGSSHSGAPDPPTLARGHNVINIVPESRAHF----FQQLGVLATLLFILLV 256  
Db 169 WRAATSSMSSPRAETSSSSWATCWPRCCSSCSWSLWSPAG----- 214  
QY 257 TVLLAARRRRRGVEYSQKSGKGDVNLAEFAVAAGDQMLYRSEDIQLDYKNNILKER 316  
Db 215 -----RGTEYSQKSGKGDVNLAEFAVAAGDQMLYRSEDIQLDYKNNILKER 265  
QY 317 AELHSPPLPAKYIDLKGRKENCK 341  
Db 266 AELHSPPLPAKYIDLKGRKENCK 290

RESULT 13

ABB10523  
ID ABB10523 standard; Protein; 192 AA.

XX ABB10523;

DT 10-JAN-2002 (first entry)

DE Human cDNA SEQ ID NO: 831.

XX Human; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorder; inflammation.

OS Homo sapiens.

XX WO200154474-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01349.

XX 31-JAN-2000; 2000US-179065P..

PR 04-FEB-2000; 2000US-180628P.  
PR 24-FEB-2000; 2000US-184664P.  
PR 02-MAR-2000; 2000US-186350P.  
PR 16-MAR-2000; 2000US-189874P.  
PR 17-MAR-2000; 2000US-190076P.  
PR 18-APR-2000; 2000US-198123P.  
PR 19-MAY-2000; 2000US-205515P.  
PR 07-JUN-2000; 2000US-209467P.  
PR 28-JUN-2000; 2000US-214886P.  
PR 30-JUN-2000; 2000US-215135P.  
PR 07-JUL-2000; 2000US-216647P.  
PR 07-JUL-2000; 2000US-216880P.  
PR 11-JUL-2000; 2000US-217487P.  
PR 11-JUL-2000; 2000US-217496P.  
PR 14-JUL-2000; 2000US-218290P.  
PR 26-JUL-2000; 2000US-220963P.  
PR 26-JUL-2000; 2000US-220964P.  
PR 14-AUG-2000; 2000US-224518P.  
PR 14-AUG-2000; 2000US-224519P.  
PR 14-AUG-2000; 2000US-225213P.  
PR 14-AUG-2000; 2000US-225214P.  
PR 14-AUG-2000; 2000US-225266P.  
PR 14-AUG-2000; 2000US-225267P.  
PR 14-AUG-2000; 2000US-225268P.  
PR 14-AUG-2000; 2000US-225270P.  
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PR 14-AUG-2000; 2000US-225757P.  
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PR 18-AUG-2000; 2000US-226279P.  
PR 22-AUG-2000; 2000US-226681P.  
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PR 22-AUG-2000; 2000US-227182P.  
PR 23-AUG-2000; 2000US-227009P.  
PR 30-AUG-2000; 2000US-228924P.  
PR 01-SEP-2000; 2000US-229287P.  
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PR 08-SEP-2000; 2000US-231243P.  
PR 08-SEP-2000; 2000US-231244P.  
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PR 08-SEP-2000; 2000US-231414P.  
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PR 08-SEP-2000; 2000US-232081P.  
PR 12-SEP-2000; 2000US-231968P.  
PR 14-SEP-2000; 2000US-232397P.  
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PR 21-SEP-2000; 2000US-234223P.  
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PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-236802P.  
PR 02-OCT-2000; 2000US-237037P.

PR 02-OCT-2000; 2000US-237038P.  
PR 02-OCT-2000; 2000US-237039P.  
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PR 20-OCT-2000; 2000US-240960P.  
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PR 20-OCT-2000; 2000US-241786P.  
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PR 01-NOV-2000; 2000US-244617P.  
PR 08-NOV-2000; 2000US-246474P.  
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PR 08-NOV-2000; 2000US-246478P.  
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PR 08-NOV-2000; 2000US-246524P.  
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PR 08-NOV-2000; 2000US-246532P.  
PR 08-NOV-2000; 2000US-246609P.  
PR 08-NOV-2000; 2000US-246610P.  
PR 08-NOV-2000; 2000US-246611P.  
PR 08-NOV-2000; 2000US-246613P.  
PR 17-NOV-2000; 2000US-249207P.  
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PR 17-NOV-2000; 2000US-249211P.  
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PR 17-NOV-2000; 2000US-249215P.  
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PR 17-NOV-2000; 2000US-249217P.  
PR 17-NOV-2000; 2000US-249218P.  
PR 17-NOV-2000; 2000US-249244P.  
PR 17-NOV-2000; 2000US-249245P.  
PR 17-NOV-2000; 2000US-249264P.  
PR 17-NOV-2000; 2000US-249265P.  
PR 17-NOV-2000; 2000US-249297P.  
PR 17-NOV-2000; 2000US-249300P.  
PR 01-DEC-2000; 2000US-250160P.  
PR 01-DEC-2000; 2000US-250391P.  
PR 05-DEC-2000; 2000US-251030P.  
PR 05-DEC-2000; 2000US-251988P.  
PR 05-DEC-2000; 2000US-256719P.  
PR 06-DEC-2000; 2000US-251479P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
PR 08-DEC-2000; 2000US-251989P.  
PR 08-DEC-2000; 2000US-251990P.  
PR 11-DEC-2000; 2000US-254097P.  
PR 05-JAN-2001; 2001US-259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476161/51.

N-PSDB; ABA06745.

Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition

XX Claim 11; SEQ ID NO: 831; 859pp + Sequence Listing; English.  
PS  
XX The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention.  
XX Sequence 192 AA;  
Query Match 52.6%; Score 955; DB 22; Length 192;  
Best Local Similarity 98.9%; Pred. No. 7.2e-78;  
Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 80  
DB 17 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 76  
QY 81 ALLTCVNRGHVWTDHRHVEEAQVQVHWDROPVPHDRADRLLDLYASGERRAYGPLEFLRD 140  
DB 77 ALLTCVNRGHVWTDHRHVEEAQVQVHWDROPVPHDRADRLLDLYASGERRAYGPLEFLRD 136  
QY 141 RVAVGADAFERGFSLRIEPLVADGEGTYSCHLHHYCGLHERRVFLHTVAEPHAE 196  
DB 137 RVAVGADAFERGFSLRIEPLVADGEGTYSCHLHHYCGLHERRVFLHTVAEPHAE 192

RESULT 14

AAU18028  
ID AAU18028 standard; Protein; 192 AA.  
XX  
AC AAU18028;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immunoglobulin polypeptide SEQ ID No 173.

XX Immunoglobulin; signal transduction pathway protein; cancer;  
OS antitense therapy; gene therapy; neurological disorder; renal disorder;  
XX cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;  
KW reproductive disorder; immune system disorder; proliferative disorder;  
KW muscular disorder.

XX Homo sapiens.

XX WO200155315-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01326.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

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PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

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PR 14-AUG-2000; 2000US-0225266.  
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PR 22-AUG-2000; 2000US-0227182.  
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PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
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PR 12-SEP-2000; 2000US-0231968.  
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PR 14-SEP-2000; 2000US-0232400.  
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PR 21-SEP-2000; 2000US-0234223.  
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PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
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PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
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PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
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PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
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PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
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PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
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PR 05-DEC-2000; 2000US-0251030.  
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PR 06-DEC-2000; 2000US-0251479.  
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PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 11-DEC-2000; 2000US-0251990.  
PR 05-JAN-2001; 2001US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX  
XX  
DR WPI; 2001-457725/49.  
XX N-PSDB; AAS28816.  
PT  
XX  
PS  
XX  
XX  
CC Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the  
CC invention. The polypeptides and their associated polynucleotides can be  
CC used to diagnose a pathological condition or a susceptibility to a  
CC pathological condition in a subject by determining the presence or  
CC absence of a mutation in a DNA sequence or determining the presence or  
CC amount of expression of the protein. Alternatively the identification of  
CC a binding partner to a sequence allows determination of changes in  
CC protein activity. The sequences can be used as research tools for  
CC receptors or other signal transduction pathway proteins that interact  
CC with the polypeptides of the invention and can be used to treat, prevent  
CC or diagnose various types of disorders such as neurological disorders,  
CC cardiovascular disorders, gastrointestinal disorders, reproductive  
CC disorders, immune system disorders, renal disorders, muscular disorders,  
CC pulmonary disorders, proliferative disorders and cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

Isolated novel immunoglobulin polypeptide for monitoring the presence and progression of diseases and for diagnosis -

Claim 11; SEQ ID No 173; 551pp; English.

```
SQ Sequence 192 AA;
Query Match 52.6%; Score 955; DB 22; Length 192;
Best Local Similarity 98.9%; Pred. No. 7.2e-78;
Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKEVLAVARGAP 80
Db 17 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKEVLAVARGAP 76

Qy 81 ALLTCVNRGHVWTDHRVVEEAQQVHVHNDRQPPGVPHDRADRLDLLYASGERRAYGFLFLRD 140
Db 77 ALLTCVNRGHVWTDHRVVEEAQQVHVHNDRQPPGVPHDRADRLDLLYASGERRAYGFLFLRD 136

Qy 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHAE 196
Db 137 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHAE 192

RESULT 15
ABP67110
ID ABP67110 standard; Protein; 192 AA.
XX
AC ABP67110;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 831.
XX
KW Human; neutrotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
US2002090672-A1.
XX
11-JUL-2002.
XX
17-JAN-2001; 2001US-0764853.
XX
31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 11-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
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PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
(ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
Rosen CA, Ruben SM, Barash SC;
PI
XX
WPI: 2002-681727/73.
N-PSDB; ABV84082.
XX
Novel polypeptide useful for diagnosis, prognosis, prevention, and
treatment of immune, hyperproliferative, renal, respiratory,
cardiovascular, reproductive, endocrine, gastrointestinal and
neurological disorders
PT
PT
PT
XX
Claim 11; SEQ ID NO 831; 369pp + Sequence Listing; English.
XX
The invention relates to novel genes (ABV83682-ABV84101) and proteins
(ABP66710-ABP67129) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (ant)agonists are useful
in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone
marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
(b) immune disorders e.g. Addison's disease, allergies, autoimmune
haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
disease, multiple sclerosis, rheumatoid arthritis and ulcerative
colitis; (c) cardiovascular disorders such as myocardial ischaemias;
(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
and parasitic infections.
CC
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 192 AA;
Query Match 52.6%; Score 955; DB 23; Length 192;
Best Local Similarity 98.9%; Pred. No. 7.2e-78;
Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKEVLAVARGAP 80
Db 17 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKEVLAVARGAP 76

Qy 81 ALLTCVNRGHVWTDHRVVEEAQQVHVHNDRQPPGVPHDRADRLDLLYASGERRAYGFLFLRD 140
Db 77 ALLTCVNRGHVWTDHRVVEEAQQVHVHNDRQPPGVPHDRADRLDLLYASGERRAYGFLFLRD 136

Qy 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHAE 196
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Db 137 RVAVGADAFERGFSLRIEPLIEVADEGTYSCHLHHYCGLHRRVFLTVAPHA 192

Search completed: February 13, 2004, 15:30:19  
Job time : 46 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:30:22 ; Search time 41 Seconds  
(without alignments)  
2146.242 Million cell updates/sec

Title: US-10-006-818A-77  
Perfect score: 1816  
Sequence: 1 MALPSRILLWKLVLLQSSAV.....SPLPAKYIDLDKGRKENCK 341

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23.\*

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID     | Description        |
|------------|--------|-------------|--------|--------|--------------------|
| 1          | 1755.5 | 96.7        | 442    | Q9BRK3 | Q9brk3 homo sapien |
| 2          | 1694.5 | 93.3        | 450    | Q96KC3 | Q96kc3 homo sapien |
| 3          | 1362.5 | 75.0        | 442    | Q920S7 | Q920s7 mus musculu |
| 4          | 1358.5 | 74.8        | 442    | Q9DBV4 | Q9dbv4 mus musculu |
| 5          | 1079.5 | 59.4        | 437    | Q90WI4 | Q90wi4 gallus gall |
| 6          | 129    | 7.1         | 686    | Q9ERS6 | Q9ers6 mus musculu |
| 7          | 126    | 6.9         | 447    | Q8NHJ6 | Q8nhj6 homo sapien |
| 8          | 123    | 6.8         | 650    | Q8NHL6 | Q8nhl6 homo sapien |
| 9          | 123    | 6.8         | 650    | Q75024 | Q75024 homo sapien |
| 10         | 122.5  | 6.7         | 651    | Q8NHJ9 | Q8nhj9 homo sapien |
| 11         | 122    | 6.7         | 652    | Q75025 | Q75025 homo sapien |
| 12         | 120.5  | 6.6         | 448    | Q8NLC7 | Q8nlc7 homo sapien |
| 13         | 119.5  | 6.6         | 448    | Q8NHL5 | Q8nhl5 homo sapien |
| 14         | 119.5  | 6.6         | 651    | Q8NHK0 | Q8nhk0 homo sapien |
| 15         | 118.5  | 6.5         | 448    | Q15468 | Q15468 homo sapien |
| 16         | 118.5  | 6.5         | 448    | Q75021 | Q75021 homo sapien |

|    |       |     |      |    |        |                    |
|----|-------|-----|------|----|--------|--------------------|
| 17 | 115.5 | 6.4 | 533  | 4  | Q8NCB6 | Q8ncb6 homo sapien |
| 18 | 115.5 | 6.4 | 534  | 4  | Q8NB18 | Q8nb18 homo sapien |
| 19 | 114   | 6.3 | 658  | 4  | Q9NZN0 | Q9nzn0 homo sapien |
| 20 | 114   | 6.3 | 686  | 4  | Q9NP60 | Q9np60 homo sapien |
| 21 | 113   | 6.2 | 1746 | 4  | Q8WY19 | Q8wy19 homo sapien |
| 22 | 112   | 6.2 | 2013 | 11 | Q8VHZ8 | Q8vzh8 rattus norv |
| 23 | 112   | 6.2 | 2013 | 11 | Q9ERC8 | Q9erc8 mus musculu |
| 24 | 111.5 | 6.1 | 915  | 11 | Q8R4B3 | Q8r4b3 mus musculu |
| 25 | 111.5 | 6.1 | 1723 | 11 | Q8CHB2 | Q8chb2 mus musculu |
| 26 | 110.5 | 6.1 | 645  | 6  | Q8MJZ5 | Q8mjz5 pan troglod |
| 27 | 110   | 6.1 | 597  | 4  | Q8NHJ8 | Q8nhj8 homo sapien |
| 28 | 109.5 | 6.0 | 1044 | 4  | Q961W3 | Q961w3 homo sapien |
| 29 | 109   | 6.0 | 1214 | 4  | Q75054 | Q75054 homo sapien |
| 30 | 108.5 | 6.0 | 336  | 6  | O18906 | O18906 macaca mula |
| 31 | 108   | 5.9 | 381  | 4  | Q9Y4A4 | Q9y4a4 homo sapien |
| 32 | 107.5 | 5.9 | 344  | 4  | Q9UKV4 | Q9ukv4 homo sapien |
| 33 | 107.5 | 5.9 | 802  | 13 | O42127 | O42127 xenopus lae |
| 34 | 107.5 | 5.9 | 1217 | 11 | P97685 | P97685 rattus norv |
| 35 | 107.5 | 5.9 | 1842 | 4  | O8IZY3 | O8izy3 homo sapien |
| 36 | 107.5 | 5.9 | 2053 | 4  | Q8WXU7 | Q8wxu7 homo sapien |
| 37 | 107.5 | 5.9 | 2053 | 4  | O8IZY4 | O8izy4 homo sapien |
| 38 | 107.5 | 5.9 | 2113 | 4  | O8TD84 | O8td84 homo sapien |
| 39 | 106.5 | 5.9 | 183  | 4  | Q9UEL6 | Q9uel6 homo sapien |
| 40 | 106.5 | 5.9 | 1041 | 4  | O94856 | O94856 homo sapien |
| 41 | 106   | 5.8 | 209  | 4  | Q9NYK4 | Q9nyk4 homo sapien |
| 42 | 105.5 | 5.8 | 243  | 4  | Q9UEL4 | Q9uel4 homo sapien |
| 43 | 105.5 | 5.8 | 598  | 4  | O8NHJ7 | O8nhj7 homo sapien |
| 44 | 105.5 | 5.8 | 598  | 4  | Q8N423 | Q8n423 homo sapien |
| 45 | 105.5 | 5.8 | 598  | 4  | O75017 | O75017 homo sapien |

#### ALIGNMENTS

##### RESULT 1

Q9BRK3 ID Q9BRK3 PRELIMINARY; PRT; 442 AA.  
AC Q9BRK3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas, and Eye;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006213; AAH06213.1; -;  
DR EMBL; BC017312; AAH17312.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 442 AA; 49131 MW; B08F89D726222CA1 CRC64;

Query Match 96.7%; Score 1755.5; DB 4; Length 442;  
Best Local Similarity 77.1%; Pred. No. 3.3e-157;  
Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;

Qy 1 MALPSRILLWKLVLLQSSAVLHLS----- 24  
Db 1 MALPSRILLWKLVLLQSSAVLHLSGSSVFPAAAGSSVSESASWEAGARVLRQCSPMV 60  
Qy 25 ----- 24  
Db 61 WTQDLHQRVLRVHWDLRGPGGPARRLLDLSAGEQRVYEARDRGRLELSASAFDQGNF 120



Qy 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 79  
Db 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 180  
Qy 80 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 139  
Db 181 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 240  
Qy 140 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 199  
Db 241 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 300  
Qy 140 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 199  
Db 241 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 300  
Qy 200 RGSPNGSSSHSGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLAATLLFILLVTVL 259  
Db 301 RGSPNGSSSHSGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLAATLLFILLVTVL 360  
Qy 260 LAARRRGGEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIDLK 319  
Db 361 LAARRRGGEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIDLK 420  
Qy 320 AHSPLPAKYIDLDKGRKENCK 341  
Db 421 AHSPLPAKYIDLDKGRKENCK 442  
RESULT 2  
Q96KC3 PRELIMINARY; PRT; 450 AA.  
AC Q96KC3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ14363.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.,  
RT "NEDO human cDNA sequencing project."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK027269; BAB55010.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 450 AA; 49606 MW; 52565CBB68B534A6 CRC64;  
Query Match 93.3%; Score 1694.5; DB 4; Length 450;  
Best Local Similarity 75.5%; Pred. No. 2e-151;  
Matches 332; Conservative 1; Mismatches 0; Indels 107; Gaps 2;  
Qy 1 MALPSRILLKVLQSSAVLHLS----- 24  
Db 1 MALPSRILLKVLQSSAVLHLS----- 60  
Qy 25 ----- 24  
Db 61 WTQDRLHQRVLRVWDLRPGGPPARLLDLLYSAGEQRYVEARDRGRLELSASFDDGNF 120  
Qy 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 79  
Db 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 180

Qy 80 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 139  
Db 181 PALLTCVNRGHVWTDHVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 240  
Qy 140 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 199  
Db 241 DRVAVGADAFERGDFFSLRIEPLVADGTYSCHLHHYCHLHERRVPHLTVAEPHAEP 300  
Qy 200 RGSPNGSSSHSGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLAATLLFILLVTVL 259  
Db 301 RGSPNGSSSHSGAPGPDPTLARGHNVINIVPESRAHFFQOLGYVLAATLLFILLVTVL 360  
Qy 260 LAARRRGGEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIDLK 313  
Db 361 LAARRRGGEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIDLK 420  
Qy 314 KERAELAHSPFLPAKYIDLDK 333  
Db 421 KERAELAHSPFLPAKYIDLDK 440  
RESULT 3  
Q920S7 PRELIMINARY; PRT; 442 AA.  
AC Q920S7  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Adipocyte-specific protein 3 (RIKEN CDNA 1200013A08 gene).  
GN 1200013A08RIK OR ASP3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tsuruga H.;  
RT "Adipocyte-specific protein 3, a novel protein upregulated during  
RT adipocyte differentiation."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB040488; BAB68501.1; -  
DR EMBL; BC026438; AAH26438.1; -  
DR MGD; MGI:1922011; 1200013A08RIK.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
SQ SEQUENCE 442 AA; 49765 MW; B129028EDB1B1844 CRC64;  
Query Match 75.0%; Score 1362.5; DB 11; Length 442;  
Best Local Similarity 61.3%; Pred. No. 4.5e-120;  
Matches 271; Conservative 21; Mismatches 49; Indels 101; Gaps 3;  
Qy 1 MALPSRILLKVLQSSAVL----- 21  
Db 1 MELLRSVLKVLQSSAVLSSGPGSTAAASNSLVSESVSLAAGTQAVLRCQSPRMV 60  
Qy 22 ----LHS----- 24  
Db 61 TQDRLHQRVLRVWDLRSGGSGQRRLVDMYSAGEQRYVEPRDRLLLSAFHDFNFS 120  
Qy 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 80  
Db 121 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 180

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QY 81 ALLTCVNRGHVWTDHVEEAQQVHWDQPPGVPHDRADRLLDLYASGERRAYGPIFLRD 140
Db 181 ALMTCINRAHVWTDHLEEAQQVHWDQRLPGVSHDRADRLLDLYASGERRAYGPIFLRD 240
QY 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGHLHRRVFLHTVAEPHAEPPPPR 200
Db 241 RVSNTNFAFGDFSLRIDELEAEGTYSCHLHHYCGHLHRRVFLHTVAEPHAEPPPPR 300
QY 201 GSPGNGSSHGAPGPDPTLARGHNVINIVIPESRAHFFQOLGYVLATLLPILLITVLL 260
Db 301 ASFGNGSGHSSAPSPDPTLTRGHSIINIVIPEDHTFFQOLGYVLATLLPILLITVLL 360
QY 261 AARRRR-GGYEYSQKSGKSGKDVNLAEFAVAAGDQMLYRSEDQLDYKNNILKERAEL 319
Db 361 ATRHSHGGCKTSDKAGKSGKDVNMVFAVATRDQAPYRTEDIQLDYKNNILKERAEL 420
QY 320 AHSPLPAKYIDLDKGRKENCK 341
Db 421 AHSPLPAKDVLDEKFRKEYCK 442

RESULT 4
Q9DBV4 PRELIMINARY; PRT; 442 AA.
AC Q9DBV4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1200013A08Rik protein.
GN 1200013A08Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tcyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004732; BAB23514.1; -.
DR MGD; MGI:1922011; 1200013A08Rik.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 442 AA; 49750 MW; 9600816B14AAA6EF CRC64;

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Query Match 74.8%; Score 1358.5; DB 11; Length 442;
Best Local Similarity 61.1%; Pred. No. 1.1e-119;
Matches 270; Conservative 22; Mismatches 49; Indels 101; Gaps 3;
QY 1 MALPSRILLWKLVLLQSSAVL----- 21

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Db 1 MELLSRVLLWKLVLLQSSAVLSSGPGSGTAAASSSLVSESVVSLAAGTQAVLRQSPRMVM 60
QY 22 ----LHS----- 24
Db 61 TQDLHQRVHWDLSGGPGSQRRRLVDMYSAGEQRVYEPDRDRLLSPSAFHDGNFS 120
QY 25 ----AVEETDAGLYTCNLHHYCHLYESLAVRLVTDGPPATPAYWDGEKEVLAVARGAP 80
Db 121 LLIRAVDRGDEGVYTCNLHHYCHLDESILAVLVEVTEPDLSSRAYWDGEKEVLVAHGAP 180
QY 81 ALLTCVNRGHVWTDHVEEAQQVHWDQPPGVPHDRADRLLDLYASGERRAYGPIFLRD 140
Db 181 ALMTCINRAHVWTDHLEEAQQVHWDQRLPGVSHDRADRLLDLYASGERRAYGPIFLRD 240
QY 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGHLHRRVFLHTVAEPHAEPPPPR 200
Db 241 RVSNTNFAFGDFSLRIDELEAEGTYSCHLHHYCGHLHRRVFLHTVAEPHAEPPPPR 300
QY 201 GSPGNGSSHGAPGPDPTLARGHNVINIVIPESRAHFFQOLGYVLATLLPILLITVLL 260
Db 301 ASFGNGSGHSSAPSPDPTLTRGHSIINIVIPEDHTFFQOLGYVLATLLPILLITVLL 360
QY 261 AARRRR-GGYEYSQKSGKSGKDVNLAEFAVAAGDQMLYRSEDQLDYKNNILKERAEL 319
Db 361 ATRHSHGGCKTSDKAGKSGKDVNMVFAVATRDQAPYRTEDIQLDYKNNILKERAEL 420
QY 320 AHSPLPAKYIDLDKGRKENCK 341
Db 421 AHSPLPAKDVLDEKFRKEYCK 442

RESULT 5
Q90WI4 PRELIMINARY; PRT; 437 AA.
AC Q90WI4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasma membrane protein 1B3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Dong S., Halfter W.;
RT "An anti cell adhesive protein from embryonic chick kidney.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373843; AAX55399.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 437 AA; 50703 MW; 398CC264A88D4711 CRC64;

Query Match 59.4%; Score 1079.5; DB 13; Length 437;
Best Local Similarity 61.1%; Pred. No. 2.4e-93;
Matches 206; Conservative 43; Mismatches 79; Indels 9; Gaps 4;
QY 6 RILLWKLVLLQSSAVLHSAVEETDAGLYTCNLHHYCHLYESLAVRLVTDGPPATPAY 65
Db 109 RILMPQNAFTDGNFSLVKDVAESDAGVYSCNLHHYCHLYETVKIQLDITKKAKAKEY 168
QY 66 WDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDQPPGVPHDRADRLLDLY 125
Db 169 WDGEKAVIVALEGSTVMLPCVNRNHIWTERHSEEQVHWDQPPGVPHDRADRLLDLY 228
QY 126 ASGERRAYGPIFLRDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGHLHRRV 185

```



OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20395285; PubMed=10941837;  
RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;  
RT "Genomic organization of the human leukocyte immunoglobulin-like  
RT receptors within the leukocyte receptor complex on chromosome  
RT 19q13.4";  
RL Immunogenetics 51:659-669(2000).  
DR EMBL; AF189277; AAC08984.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00408; IGC2; 3.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Immunoglobulin domain; Receptor.  
SQ SEQUENCE 650 AA; 70819 MW; 549196EA4ED2767C CRC64;  
  
Query Match 6.8%; Score 123; DB 4; Length 650;  
Best Local Similarity 20.6%; Pred. No. 0.0098;  
Matches 68; Conservative 39; Mismatches 105; Indels 118; Gaps 12;  
  
QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHHWDROP 110  
Db 326 VLSVQPGP-----TVASGENVTLLCQSQGWMQTFLLTKEGAADDPW---- 367  
  
QY 111 PGVPHDRADRLDLYASGERRAYGFLFDRVAVGADAFERGFSLRIEPLVADGTYS 170  
Db 368 -----RLRSTYQSKYQAEFFM-----GPTSAHAGTYR 396  
  
QY 171 CH----LHHYCGLHERRVFLHTVAEPHAEPPRPGSPGNGSSHGAPGDPPTLARGHNVIN 227  
Db 397 CYGQSSKPYLLTHPSDPLELVVSGSGP---SSPTTGTSTSGPEDQLTPTGSD--- 450  
  
QY 228 VIVPES--RAHFFQQLGYVLATLLFILLVTLAARRRGYEDQSKGSKGKDVN 285  
Db 451 ---PQSLGLRHGVIGILVAVILLLLLLFLLRHRQGHWTSTQK----- 498  
  
QY 286 LAEFAVAAG-----DQMLYRS-----EDIQLDYKN----- 310  
Db 499 -ADFQHPAGAVGPEPTDRGLQWRSSPAADAQEENLYAAVKHTQPEDGVEMDTRSPHDEDP 557  
  
QY 311 -----NILKERAEALAH--SPLPAKYID 330  
Db 558 QAVTYAEVKHSRPRREMASPPSPSLSGEFLD 587  
  
RESULT 9  
O75024 PRELIMINARY; PRT; 650 AA.  
AC O75024;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Leucocyte immunoglobulin-like receptor-1 (leukocyte immunoglobulin-  
DE like receptor, subfamily B (with TM and ITIM domains), member 1).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,  
RA Hsu M.L.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells from Tonsils;  
RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF009220; AAB63521.1; -.  
DR EMBL; BC015731; AAH15731.1; -.  
DR HSSP; P43626; INKR.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Receptor.  
SQ SEQUENCE 650 AA; 70816 MW; DL321C0982B448CA CRC64;  
  
Query Match 6.8%; Score 123; DB 4; Length 650;  
Best Local Similarity 20.6%; Pred. No. 0.0098;  
Matches 68; Conservative 39; Mismatches 105; Indels 118; Gaps 12;  
  
QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHHWDROP 110  
Db 326 VLSVQPGP-----TVASGENVTLLCQSQGWMQTFLLTKEGAADDPW---- 367  
  
QY 111 PGVPHDRADRLDLYASGERRAYGFLFDRVAVGADAFERGFSLRIEPLVADGTYS 170  
Db 368 -----RLRSTYQSKYQAEFFM-----GPTSAHAGTYR 396  
  
QY 171 CH----LHHYCGLHERRVFLHTVAEPHAEPPRPGSPGNGSSHGAPGDPPTLARGHNVIN 227  
Db 397 CYGQSSKPYLLTHPSDPLELVVSGSGP---SSPTTGTSTSGPEDQLTPTGSD--- 450  
  
QY 228 VIVPES--RAHFFQQLGYVLATLLFILLVTLAARRRGYEDQSKGSKGKDVN 285  
Db 451 ---PQSLGLRHGVIGILVAVILLLLLLFLLRHRQGHWTSTQK----- 498  
  
QY 286 LAEFAVAAG-----DQMLYRS-----EDIQLDYKN----- 310  
Db 499 -ADFQHPAGAVGPEPTDRGLQWRSSPAADAQEENLYAAVKHTQPEDGVEMDTRSPHDEDP 557  
  
QY 311 -----NILKERAEALAH--SPLPAKYID 330  
Db 558 QAVTYAEVKHSRPRREMASPPSPSLSGEFLD 587  
  
RESULT 10  
Q8NHJ9 PRELIMINARY; PRT; 651 AA.  
AC Q8NHJ9;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Leukocyte immunoglobulin-like receptor-1.  
GN LILRB1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Canavez F.C.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283985; AAL36989.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00408; IGC2; 3.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Immunoglobulin domain; Receptor.  
SQ SEQUENCE 651 AA; 70906 MW; C85BCCD7CD9996BB CRC64;  
  
Query Match 6.7%; Score 122.5; DB 4; Length 651;  
Best Local Similarity 21.9%; Pred. No. 0.011;  
Matches 73; Conservative 35; Mismatches 102; Indels 123; Gaps 14;  
  
QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHHWDROP 110

Db 326 VLSVQPGP-----TVASGENVTLLCQSQWMQTFLLTKEGAADDPW----- 367  
QY 111 PGVPHDRADRLDLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTVS 170  
Db 368 -----RLRSTYQSQYQAEFFM-----GPTSAHAGTYR 396  
QY 171 CH--LHHYCGLHERRVFLHTVAEPHAEPGRPGNG-SSHSAGPDPDTLARGHNV 226  
Db 397 CYGSQSKPYLLTHPSDPLELVSGPSGGP---SSPTTGTSTAGPEDQPLTPTGSD-- 451  
QY 227 NVIVPES--RAHFFQQLGVVLTATLLFILLVTVLLAARRRRGGYEDQSGSKGKDV 284  
Db 452 ----PQGLGRHLGVVIGILVAVILLLLLLLLFLLLRHRRQKHTWTQK----- 499  
QY 285 NLAFAVAAG-----DQMLY-----RSED 303  
Db 500 --ADFQHPAGVGPETDRGLQWRSSPAADAQENLYAAVKHTQPEDGVEMDTRSPHDE 557  
QY 304 IQ----LDYKNNILKERAELAH--SPLPAKYID 330  
Db 558 LQAVTYAEVKHS--RPRREMASPPPLSGEFLD 588

RESULT 11

ID O75025 PRELIMINARY; PRT; 652 AA.  
AC O75025;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leucocyte immunoglobulin-like receptor-1.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,  
RA Hsu M.L.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF009221; AAB63522.1; -.  
DR HSSP; P43626; 1NKR.  
DR Genew; HGNC:6605; LILRB1.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
SQ SEQUENCE 652 AA; 71018 MW; 93AF8F021A22949D CRC64;

Query Match 6.7%; Score 122; DB 4; Length 652;  
Best Local Similarity 21.4%; Pred. No. 0.012;  
Matches 71; Conservative 37; Mismatches 104; Indels 120; Gaps 13;

QY 51 VRLEVTGPPATPAYWDGEKVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHVDRQP 110  
Db 326 VLSVQPGP-----TVASGENVTLLCQSQWMQTFLLTKEGAADDPW----- 367  
QY 111 PGVPHDRADRLDLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTVS 170  
Db 368 -----RLRSTYQSQYQAEFFM-----GPTSAHAGTYR 396  
QY 171 CH--LHHYCGLHERRVFLHTVAEPHAEPGRPGNG-SSHSAGPDPDTLARGHNV 226  
Db 397 CYGSQSKPYLLTHPSDPLELVSGPSGGP---SSPTTGTSTAGPEDQPLTPTGSD-- 451  
QY 227 NVIVPES--RAHFFQQLGVVLTATLLFILLVTVLLAARRRRGGYEDQSGSKGKDV 284  
Db 452 ----PQGLGRHLGVVIGILVAVILLLLLLLLFLLLRHRRQKHTWTQK----- 499  
QY 285 NLAFAVAAG-----DQMLYRS-----EDIQIDYKNNILKE 315

Db 500 --ADFQHPAGVGPETDRGLQWRSSPAADAQENLYAAVKHTQPEDGVEMDTRSPHDE 557  
QY 316 -----RAELAH-----SPLPAKYID 330  
Db 558 DPQAVTYAEVKHSRPRREMASPPPLSGEFLD 589  
RESULT 12  
ID Q8NIC7 PRELIMINARY; PRT; 448 AA.  
AC Q8NIC7;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leucocyte immunoglobulin-like receptor, subfamily B (With TM and ITIM domains), member 4.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straussberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC026309; AAH26309.1; -.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 2.  
KW Receptor.  
SQ SEQUENCE 448 AA; 49303 MW; A6155D29E7D89812 CRC64;

Query Match 6.6%; Score 120.5; DB 4; Length 448;  
Best Local Similarity 21.9%; Pred. No. 0.01;  
Matches 87; Conservative 40; Mismatches 131; Indels 139; Gaps 20;

QY 48 SLAVRLEVTGPPATPAYWDGEKVLAVARGAPALLTCVNRGHVW-----TDHVEEA 100  
Db 14 SLGPRTDMQAGPLPKPTLWAEPPGVSISWG-----NSVTWCQQTLEAREYLDKE 63  
QY 101 QQVHVDRQPPGVPHDRA-----DRLLDLYASGERRAY-----GPLEFLDRVAVG 145  
Db 64 ESPAPWDRQNPLEPKNKARFSPISMTEDYA-GYRCYRSPVGSQSPDPLEL---VMTG 119  
QY 146 A-----DAF-----ERGFSL----- 156  
Db 120 AYSKPTLSALPSPLVTSGKSVTLCCSRSPMDTFLLIKERAAPHLLHLRSEHGAQQHQA 179  
QY 157 -RIEPLVADGTYTCHLHH---HYCGLHERRVFLHTVAEPHAEPGRPGSPGNGSSHGA 212  
Db 180 FPMSPVTSVHGTYRCFSHGSHYLLSHPSDPLELIVS--GSLEGPRSPSTRSVSTAAG 237  
QY 213 PGPDPTLARGHNVINIVIPES--RAHFFQQLGVVLTATLLFILLVTVL-----L 260  
Db 238 PEDQPLMPTGS-----VPHSGLRRHWEVLIGVLVVSILLLSLLFLLLOHWRQGHRTL 291  
QY 261 AAR-----RRGGYEYSDQSG-----KSKGKDVNLAFAVAAGDQMLYRSED-IQLDYKN 310  
Db 292 AQRQADFORPPGAEPKDGGLQRRSSPAADVQGENFCAAVKNT---QPEDGVEMDTRQ 348  
QY 311 NILKE-----RAELAH--SPLPAKYID 330  
Db 349 SPHEDDPQAVTYAKVKHSRPRREMASPPPLSGEFLD 385

RESULT 13

ID Q8NHL5 PRELIMINARY; PRT; 448 AA.  
AC Q8NHL5;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leucocyte immunoglobulin-like receptor 5.  
GN LIR5.





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QY 101 QQVHWDRQPPGVPHDRA---DRLLDLYASGERRAY-----GPLFLRDRVAVG 145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 ESPAPWDRQNPUEPKNARFISFMTEDYA-GRYRCYRSPVWGSQPSDDLEL---VMTG 119
QY 146 A-----DAF-----ERGDPSL----- 156
Db 120 AYSKPTLSALPSPLVTSKSVTLQCQSRSPMDTFLIKERAAHPLLHLRSEHGAQQHOAE 179
QY 157 -RIEPLVADGTYSCHLHH---HYCGLHERRVFLHTVAEPHAEPPRGSPGNGSSHGA 212
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
180 FPMSPVTSVHGTYRCFSHGHFHYLLSHPSDPLELVS--CSLEGPRPSPTRSVSTAAG 237
QY 213 PGPDPTLARGHNVINVIIPES--RAHFFQOLGYVLATLLFILLVTVL-----L 260
Db 238 PEDQPLMPTGS-----VPHSGLRRHWEVLIGVLVVSILLSLLLFLLLQHWKQKRTL 291
QY 261 AAR-----RRRGVEYSDQSG-----KSKGDVNLAEFAVAAGDQMLYRSED-IQLDYKN 310
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
292 AQRQADFQRPFGAAEPEPKDGGQLQRRSSPAADVQGENFCAAVKNT---QPEDGVEMDTRQ 348
QY 311 NILKE-----RAELAH--SELPKAYID 330
Db 349 SPHDEDPQAVTYAKVKHSRPRREMAASPPPLSGEFLD 385
```

Search completed: February 13, 2004, 15:34:42  
Job time : 43 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model  
Run on: February 13, 2004, 15:30:52 ; Search time 21 Seconds  
(without alignments)  
1561.596 Million cell updates/sec

Title: US-10-006-818A-77  
Perfect score: 1816  
Sequence: 1 MALPSRILLWKLVLLQSSAV.....SPLPAKYIDLDKGRKENCX 341

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID       | Description        |
|------------|-------|---------------|--------|----------|--------------------|
| 1          | 113   | 6.2           | 1896   | 2 T08851 | Down syndrome cell |
| 2          | 112   | 6.2           | 404    | 1 I61596 | advanced glycosyla |
| 3          | 111.5 | 6.1           | 233    | 2 JC5322 | p53 specific singl |
| 4          | 105   | 5.8           | 423    | 2 T29549 | hypothetical prote |
| 5          | 105   | 5.8           | 1273   | 2 T42405 | sax-3 protein - Ca |
| 6          | 104.5 | 5.8           | 365    | 2 JC7780 | coxackie- and ade  |
| 7          | 104   | 5.7           | 111    | 2 E53285 | Ig kappa chain v a |
| 8          | 100.5 | 5.5           | 246    | 2 T01073 | T cell surface gly |
| 9          | 100.5 | 5.5           | 498    | 2 S11246 | LAG-3 protein prec |
| 10         | 100.5 | 5.5           | 2222   | 2 T13924 | sdh protein - frui |
| 11         | 99.5  | 5.5           | 111    | 2 D45722 | anti-glycoprotein  |
| 12         | 99.5  | 5.5           | 246    | 2 D46482 | T-cell surface gly |
| 13         | 99    | 5.5           | 310    | 2 D70745 | hypothetical prote |
| 14         | 98    | 5.4           | 358    | 2 A54265 | CCAAT/enhancer-bin |
| 15         | 97.5  | 5.4           | 1021   | 2 T39207 | leukocyte surface  |
| 16         | 97    | 5.3           | 394    | 2 A70979 | hypothetical prote |
| 17         | 97    | 5.3           | 3198   | 2 A43426 | collagen alpha 2 f |
| 18         | 96.5  | 5.3           | 321    | 2 D39371 | Ig V-region-like B |
| 19         | 96.5  | 5.3           | 1033   | 2 S19247 | cell adhesion prot |
| 20         | 96.5  | 5.3           | 1070   | 2 JC4593 | protein-tyrosine k |
| 21         | 96    | 5.3           | 224    | 2 I37243 | CMRF-35 antigen -  |
| 22         | 96    | 5.3           | 841    | 2 JC5894 | killer cell inhibi |
| 23         | 95.5  | 5.3           | 210    | 2 E46482 | T-cell surface gly |
| 24         | 95.5  | 5.3           | 221    | 2 C46482 | T-cell surface gly |
| 25         | 95.5  | 5.3           | 1232   | 2 T43027 | neural cell adhesi |
| 26         | 95    | 5.2           | 1268   | 1 A39640 | neural cell adhesi |
| 27         | 94.5  | 5.2           | 240    | 2 A39016 | T-cell surface gly |
| 28         | 94    | 5.2           | 95     | 2 S25177 | Ig kappa chain V r |
| 29         | 94    | 5.2           | 2761   | 2 T29285 | hypothetical prote |

|    |      |     |      |          |                    |
|----|------|-----|------|----------|--------------------|
| 30 | 93.5 | 5.1 | 101  | 2 S59640 | Ig light chain V r |
| 31 | 93.5 | 5.1 | 1051 | 2 A39712 | kinase-like protei |
| 32 | 93.5 | 5.1 | 3707 | 2 S18252 | heparan sulfate pr |
| 33 | 93   | 5.1 | 105  | 2 S44125 | Ig lambda chain V  |
| 34 | 93   | 5.1 | 129  | 2 S44114 | Ig heavy chain V r |
| 35 | 93   | 5.1 | 395  | 2 I49575 | CCAAT/enhancer bin |
| 36 | 92.5 | 5.1 | 102  | 2 PH1077 | Ig light chain V r |
| 37 | 92.5 | 5.1 | 111  | 2 A33936 | Ig kappa chain V r |
| 38 | 92.5 | 5.1 | 303  | 2 S23440 | hypothetical prote |
| 39 | 92.5 | 5.1 | 340  | 2 JC7505 | brain link protein |
| 40 | 92.5 | 5.1 | 4391 | 2 A38096 | perlecan precursor |
| 41 | 92   | 5.1 | 461  | 1 A46077 | steroid hormone re |
| 42 | 92   | 5.1 | 1344 | 2 T14316 | rig-1 protein - mo |
| 43 | 91.5 | 5.0 | 111  | 1 KVMS13 | Ig kappa chain V r |
| 44 | 91.5 | 5.0 | 115  | 2 S63596 | Ig kappa chain V r |
| 45 | 91.5 | 5.0 | 131  | 1 KVMSM6 | Ig kappa chain pre |

ALIGNMENTS

RESULT 1

T08851  
Down syndrome cell adhesion protein 1 - human (fragment)  
N;Alternate names: Down syndrome cell adhesion molecule  
C;Species: Homo sapiens (man)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C;Accession: T08851  
R;Yamakawa, K.; Huo, Y.K.; Haendel, M.A.; Hubert, R.; Chen, X.N.; Lyons, G.E.; Korenber  
submitted to the EMBL Data Library, September 1997  
A;Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down s  
A;Reference number: Z16495  
A;Accession: T08851  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1896 <YAM>  
A;Cross-references: EMBL:AF023449; NID:G3169765; PID:G3169766  
A;Experimental source: brain; developmental stage: 14 weeks; fetal  
C;Genetics:  
A;Gene: DSCAM  
A;Map position: 21q22  
A;Note: derived from alternately-spliced mRNA  
C;Function:  
A;Description: involved in nervous system development  
C;Keywords: alternative splicing

Query Match 6.2%; Score 113; DB 2; Length 1896;  
Best Local Similarity 23.0%; Pred. No. 0.6;  
Matches 45; Conservative 33; Mismatches 62; Indels 56; Gaps 9;

|    |     |  |
|----|-----|--|
| Qy | 11  | KLVLQSSAVLLHSAVEETDAGLYTCNLHHY-----CHLYESLAVRLEVTGPPATPAY 65     |
| Db | 728 | RIQVLSNGSLIKHVVEE-DSGYLCKVSNVGVADSVKSMYLTVKIPAMITSPNTTLAT 786    |
| Qy | 66  | WDGEKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQQVVHWDROPFGVPHDRADRLDLY 125 |
| Db | 787 | QGQKEMSCSTAAG-----EKPIIVRWEKE-----DRIIN-- 815                    |
| Qy | 126 | ASGERRAYGFLFLDRVA---VGADAFERGDFSLRIEPLVDEGTYSCHLHHYCGLHE 182     |
| Db | 816 | -----PEMARVLVSTKEVGEVIS---TLQILPTVREDSGFFSCHAINSYG--ED 860       |
| Qy | 183 | RRVPHLTVAEPHAEPP 198   |
| Db | 861 | RGIQLTVQEP-PDPP 875  |

RESULT 2

I61596  
advanced glycosylation end-products receptor precursor - human  
N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein  
C;Species: Homo sapiens (man)  
C;Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999



Db 279 -----GLRIERVQSDGEYVCYARNP-AGTLEASA-HLRVQAPP 316

QY 194 --HAEPPTGSGNGSSH-----SGAGP 215

Db 317 SFQTKPADQSVFAGGTATFECTLVGPSP 345

RESULT 5

T42405

sax-3 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000

C:Accession: T42405

R:Zallen, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A:Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A:Reference number: Z22160; MUID:98117250; PMID:9458046

A:Accession: T42405

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1273 <ZAL>

A:Cross-references: EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:G2804780

C:Genetics:

A:Note: sax-3

C:Function:

A:Description: sax-3 function is required at the time of axon guidance

Query Match 5.8%; Score 105; DB 2; Length 1273;

Best Local Similarity 23.4%; Pred. No. 1.7;

Matches 49; Conservative 27; Mismatches 79; Indels 54; Gaps 9;

QY 15 LOSAVALHSAVEETAGLYTCLNHLHHYCHLYESLAVRLVETDGPATPAYWDGEKEVLA 74

Db 184 LHSQGNLIIDPDRSGTYQCVANNMVGERSNPA-RLSVFEKPK-----FEQEPKDMT 237

QY 75 VARGAPALLTCVNRGHVWTDHVEEAQQVVDHROPVPHDRADRLDLVYASGERRAYG 134

Db 238 VDVGAAVLFD-----RVTDGPQPOITWKRKNPMPVTRA-----YIAKDNR--- 279

QY 135 PLFLRDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVHFLTVAEP- 193

Db 280 -----GLRIERVQSDGEYVCYARNP-AGTLEASA-HLRVQAPP 317

QY 194 --HAEPPTGSGNGSSH-----SGAGP 215

Db 318 SFQTKPADQSVFAGGTATFECTLVGPSP 346

RESULT 6

JC7780

coxsackie- and adenovirus receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 02-Apr-2002 #sequence\_revision 02-Apr-2002 #text\_change 02-Apr-2002

C:Accession: JC7780

R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto

A:Reference number: JC7780

A:Contents: Liver

A:Accession: JC7780

A:Molecule type: mRNA

A:Residues: 1-365 <THO>

A:Cross-references: GB:AY033651

C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 5.8%; Score 104.5; DB 2; Length 365;

Best Local Similarity 20.1%; Pred. No. 0.44;

Matches 55; Conservative 48; Mismatches 90; Indels 81; Gaps 13;

QY 70 KEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVVDHROPVPHDRADRLDLVYASGE 129

Db 26 EQMIEKAGETAYLPC-----KFTLGPEDQGLDIEWLLSP--ADNQKVDQVILLY-SGD 77

QY 130 RRAYGPLF--LRDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVH 187

Db 78 -KIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQSLDGTGYQCKV-KKAPGVGNKKIQL 135

QY 188 LTVARP-----HAEP-----PPRGSP 203

Db 136 TVLVKPSGIRCYVDGSEBEIGNDFKLKCEPKESGLPLRYEWQKLSQKLPSTWLPMTSP 195

QY 204 -----GNGSSHSGA-----PGDPPTLARGHNVINIVPESRAHFFQQLGYVLATLL 250

Db 196 VISVKNASAEYSGTYTCTVNRVSGDQCLLR-----LDVPPSNRAGTI--AGAVIGTLLA 249

QY 251 FILLVTVLLAARRRRRGYYSQKSGKSGKMDV 284

Db 250 LVLIALLIVFCCHKRR-----EEKYEKEVHHDI 277

RESULT 7

E53285

Ig kappa chain V and J regions, monoclonal antibody OHP 4B2.2.1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C:Accession: E53285

R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

Mol. Immunol. 28, 1063-1072, 1991

A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary stru

and their pH-reactivity profiles.

A:Reference number: A53285; MUID:92017897; PMID:1922102

A:Accession: E53285

A:Status: preliminary

A:Molecule type: DNA; protein

A:Residues: 1-111 <SAW>

A:Cross-references: GB:D12731; NID:G220542; PIDN:BAA02223.1; PID:G220543

A:Note: sequence extracted from NCBI backbone (NCBIN:63307, NCBI:63311)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F16-94/Domain: immunoglobulin homology <IMM>

Query Match 5.7%; Score 104; DB 2; Length 111;

Best Local Similarity 29.1%; Pred. No. 0.12;

Matches 34; Conservative 15; Mismatches 40; Indels 28; Gaps 5;

QY 55 VTDGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVVDHROPVGP 114

Db 4 VTQSPAS-----LAVSLQGRATVSC--RASESVDRY---GNFIHWYQKPGQP 47

QY 115 HDRADRLDLVYASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADGTYSC 171

Db 48 ----PQLLIYFASNLKSGVPARF-----SGSGRTDTLTIDPVEADDAATYTC 92

RESULT 8

T01073

T cell surface glycoprotein CD8 beta 1 chain, membrane-bound type M-2 - human

C:Species: Homo sapiens (man)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 21-Jul-2000

C:Accession: T01073

R:Nakayama, K.; Kawachi, Y.; Tokito, S.; Minami, N.; Yamamoto, R.; Imai, T.; Gachelin,

J. Immunol. 148, 1919-1927, 1992

A:Title: Recent duplication of the two human CD8 beta chain genes.

A:Reference number: A46482; MUID:92176658; PMID:1541829

A:Accession: T01073

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-246 <NAK>

A:Cross-references: EMBL:S87083; NID:G246739; PIDN:AAB21671.2; PID:G5705881

C:Genetics:

A:Gene: CD8-beta1.2

A:Introns: 15/1; 135/1; 165/1; 195/1; 207/2

C:Superfamily: T-cell surface glycoprotein CD8 beta chain; immunoglobulin homology

Query Match 5.5%; Score 100.5; DB 2; Length 246;

Best Local Similarity 22.8%; Pred. No. 0.6;

Matches 57; Conservative 32; Mismatches 96; Indels 65; Gaps 10;

QY 45 LYESLAVRLEVTGPPA--TPAYWDEGEVLAARGAPALLTCVNRGHVWTDHRHVEAQ 101  
Db 5 LWLLAAQLTVLHNSVLTQTPAY-----IKVQTNKMWLSC-----EAKISLSN 49

QY 102 QVHVDRQPPGVPHDRADRLLDLYASGERRAYGFLPLDRVAVGADAFERGFSLRIEPL 161  
Db 50 MRIYLRQRPQSSDSHHEFLALWDSAKGTHGEEVEQEKIARFRDA---SRFILNLTSV 106

QY 162 EVADECTYSCHLHHYCGLHERRVFLHTVAEPHAPPPRGSP-----GNGSSHS----- 210  
Db 107 KPDSGIYFCMI-----VGSPELTFKGTQLSVVDPLPT 140

QY 211 -GAPGDPPTLARGHNVINIVPESRAHFFQ--LGVVLA-TLLLFILLVTVLLAARRR 265  
Db 141 TAQPTKSTLKK--RVCRLPRPETQKGPLCSPITLGLLVAGVLVLLVSLGVAILHLCRRR 198

QY 266 RGGYEYSDQK 275  
Db 199 RARLRFWKQK 208

RESULT 9  
S11246  
LAG-3 protein precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 04-Mar-2000  
C:Accession: S11246  
R:Triebel, F.; Jitsukawa, S.; Baixeras, E.; Roman-Roman, S.; Genevee, C.; Viegas-Pequign  
J. Exp. Med. 171, 1393-1405, 1990  
A:Title: LAG-3, a novel lymphocyte activation gene closely related to CD4.  
A:Reference number: S11246; MUID:90237736; PMID:1692078  
A:Accession: S11246  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-498 <TRI>  
A:Cross-references: EMBL:X51985  
A:Note: the author translated the codon CCA for residue 388 as Arg  
C:Genetics:  
A:Gene: GDB:LAG3  
A:Cross-references: GDB:127449; OMIM:153337  
A:Map position: 12p13.3-12p13.3  
C:Superfamily: human LAG-3 protein  
C:Keywords: transmembrane protein

Query Match 5.5%; Score 100.5; DB 2; Length 498;  
Best Local Similarity 26.6%; Pred. No. 1.4;  
Matches 46; Conservative 9; Mismatches 69; Indels 49; Gaps 5;

QY 60 PATPAYWDEGEVLAARGAPALLTC-----VNRGHVWTDHRHVEAQVHVWDR 108  
Db 19 PVKPLQPGAEVVPVWQAQAPALPCSPITPLQDLSLRRAG-----VTWQH 65

QY 109 QP-----PGV-----PHDRADRLLDLYASGERRAYGFLPLDRVAVG 145  
Db 66 QPDSGPPAAAPGHPHAPGPPAPSSWGPRPRRYTVLSVGPGLRS--GRLPLQPRVQLD 123

QY 146 ADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHAPPP 198  
Db 124 ERGRQGRDFSLWLRPARRADAGEYRAAHLDRALSCRLRLRGLQASMTASPP 176

RESULT 10  
T13924  
sdk protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000  
C:Accession: T13924  
R:Nguyen, D.N.; Liu, Y.; Litsky, M.L.; Reinke, R.  
submitted to the EMBL Data Library, February 1997  
A:Description: Sidekick, a member of the immunoglobulin superfamily, is required for pat  
A:Reference number: Z17809

A:Accession: T13924  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2222 <NGU>  
A:Cross-references: EMBL:U88578; NID:g4099554; PID:g4099555; PIDN:AAD09632.1  
C:Genetics:  
A:Gene: sdk  
A:Cross-references: FlyBase:FBgn0021764

Query Match 5.5%; Score 100.5; DB 2; Length 2222;  
Best Local Similarity 24.8%; Pred. No. 8;  
Matches 54; Conservative 24; Mismatches 81; Indels 59; Gaps 10;

QY 13 VLLQSAVLLHSAVEETDAGLYTCNLHH-----YCHLYESLAVRLEVTGPPATPAYWDG 68  
Db 502 VQILESGDLLISNIRSDAPLYICVRANEAGSVKAEAYLSVLVRTQIIQPPVDT----- 555

QY 69 EKEVLAVARGAPALLTCVNRGHVWTDHRHVEAQVHVWDRQPPGVPHDRADRLLDLYASG 128  
Db 556 -----TVLLGLTATLQC-----KVSSD-----PSVPYN-----IDWYREG 585

QY 129 ERRAYGFLPLDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVFLH 188  
Db 586 QSST--PISNSQIRIGVQADG-----QLEIQAVRASDVGSYACVVTSP--GGNETRAARL 635

QY 189 TVAE-----PHAE-----PPRGSPGNGSSHSGAPGDDP 217  
Db 636 SVIELPPPPSNVVKVERLPEPQQASINVSWTGFGDGNP 673

RESULT 11  
D45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 109) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: D45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasc  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on t  
A:Reference number: A45722; MUID:93100833; PMID:7677958  
A:Accession: D45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-111 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBI:120592)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 5.5%; Score 99.5; DB 2; Length 111;  
Best Local Similarity 31.3%; Pred. No. 0.28;  
Matches 31; Conservative 13; Mismatches 38; Indels 17; Gaps 4;

QY 73 LAVARGAPALLTCVNRGHVWTDHRHVEAQVHVWDRQPPGVPHDRADRLLDLYASGERRA 132  
Db 11 LAVSRGQRATISC--RASESDSY---GKSFHWYQQKFGQP-----PKLLIYLASNLESG 61

QY 133 YGPIFLPLDRVAVGADAFERGFSLRIEPLVADGTYSC 171  
Db 62 VPTRF-----SGSGSRDTFTLTIDFVEADDAATYTC 92

RESULT 12  
D46482  
T-cell surface glycoprotein CD8 beta-1 chain, membrane form 2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C:Accession: D46482  
R:Nakayama, K.; Kawachi, Y.; Tokito, S.; Minami, N.; Yamamoto, R.; Imai, T.; Gachelin,  
J. Immunol. 148, 1919-1927, 1992  
A:Title: Recent duplication of the two human CD8 beta-chain genes.  
A:Reference number: A46482; MUID:92176658; PMID:1541829  
A:Accession: D46482





A;Molecule type: mRNA  
A;Residues: 1-1021 <RES>  
A;Cross-references: EMBL:Z33642; NID:9854194; PID:9854195  
C;Genetics:  
A;Gene: GDB:V7  
A;Cross-references: GDB:702141  
A;Map position: lp13-lp13  
C;Superfamily: human leukocyte surface protein V7

|                       |  |        |                  |                 |                      |
|-----------------------|--|--------|------------------|-----------------|----------------------|
| Query Match           |  | 5.4%;  | Score 97.5;      | DB 2;           | Length 1021;         |
| Best Local Similarity |  | 22.4%; | Pred. No. 5.7;   | Mismatches 106; | Indels 103; Gaps 17; |
| Matches               |  | 72;    | Conservative 40; |                 |                      |

  

|    |      |   |      |
|----|------|---|------|
| Qy | 26   | VEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWD--GEK-----EVLAVARG  | 78   |
| Db | 768  | VEDSDRGKYHC-----AVEEWLLSTNGTWHKLGKSKGLTELKLPKG              | 810  |
| Qy | 79   | APALLTCVNRGHVWTDHVEEAQQVV-----HWDQPPG---VPHDR               | 117  |
| Db | 811  | SKRVSKV-----YWTENTTEHREVAIRCLESVGSSATLYSVWYWNRENSGSKLLVHLQ  | 866  |
| Qy | 118  | ADRLLDLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPLLEVADEGTYSK-----H | 172  |
| Db | 867  | HDGLLE-----YGBGLRGHLHCYRSS--STDFVLKLHQMVEDAGMYWCRVAEWQ      | 915  |
| Qy | 173  | LHHYHC-GLHERRVFHLTVAPHAEPFPPRGSPGNGSSHSGAPGPDPTLARGHNVINVIP | 231  |
| Db | 916  | LGHPSKWINKHPMSHSGWCSPCCLOSPRFLPGS-----APRP-PLL-----         | 956  |
| Qy | 232  | ESRAHFFQQLGYVLATLLLFILLVTVLLAARRRRRGYEYSQKSG--KSKGKDNVLAEP  | 289  |
| Db | 957  | -----YF-----LFICPFVLLLLLSLLCLLYWKAR---KLSTLRNTRKEKALWVDLKE- | 1003 |
| Qy | 290  | AVAAGDQMLYRSEDIQLDYKN                                       | 310  |
| Db | 1004 | ---AGGVTTNRRDEEEDEN   | 1021 |

Search completed: February 13, 2004, 15:35:15  
Job time : 22 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:16:02 ; Search time 17 Seconds  
(without alignments)  
943.300 Million cell updates/sec

Title: US-10-006-818A-77  
Perfect score: 1816  
Sequence: 1 MALPSRILLWKLVLQSSAV.....SPLPAKYIDLKGFRENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID        | Description        |
|------------|-------|-------|--------|--------------|--------------------|
| 1          | 113   | 6.2   | 2012   | 1 DSCA_HUMAN | O60469 homo sapien |
| 2          | 112   | 6.2   | 404    | 1 RAGE_HUMAN | Q15109 homo sapien |
| 3          | 108.5 | 6.0   | 319    | 1 A33_HUMAN  | Q99795 homo sapien |
| 4          | 107.5 | 5.9   | 365    | 1 CXAR_HUMAN | P78310 homo sapien |
| 5          | 104   | 5.7   | 458    | 1 CD4_MACNE  | Q08340 macaca neme |
| 6          | 100.5 | 5.5   | 525    | 1 LAG3_HUMAN | P18627 homo sapien |
| 7          | 99    | 5.5   | 310    | 1 Y497_MYCTU | Q11162 mycobacteri |
| 8          | 98.5  | 5.4   | 300    | 1 JAM1_MOUSE | O88792 mus musculu |
| 9          | 98    | 5.4   | 358    | 1 CEBA_RAT   | P05554 rattus norv |
| 10         | 97    | 5.3   | 391    | 1 P53_MARMO  | Q36006 marmota mon |
| 11         | 97    | 5.3   | 458    | 1 CD4_MACFA  | P79185 macaca fasc |
| 12         | 97    | 5.3   | 458    | 1 CD4_MACTU  | P79184 macaca fusc |
| 13         | 96.5  | 5.3   | 1070   | 1 PTK7_HUMAN | Q13308 homo sapien |
| 14         | 96    | 5.3   | 224    | 1 CM35_HUMAN | Q08708 homo sapien |
| 15         | 95.5  | 5.3   | 210    | 1 CD8B_HUMAN | P10966 homo sapien |
| 16         | 95.5  | 5.3   | 458    | 1 CD4_CERAE  | Q08338 cercopithe  |
| 17         | 95    | 5.2   | 1284   | 1 NRCA_CHICK | P35331 gallus gall |
| 18         | 94.5  | 5.2   | 240    | 1 CD7_HUMAN  | P09564 homo sapien |
| 19         | 94    | 5.2   | 458    | 1 CD4_MACMU  | P16003 macaca mula |
| 20         | 93.5  | 5.1   | 1051   | 1 PTK7_CHICK | Q91048 gallus gall |
| 21         | 93.5  | 5.1   | 3707   | 1 PGBM_MOUSE | Q05793 mus musculu |
| 22         | 93    | 5.1   | 359    | 1 CEBA_MOUSE | P53566 mus musculu |
| 23         | 92.5  | 5.1   | 303    | 1 HYPB_AZOV1 | P31880 azotobacter |
| 24         | 92.5  | 5.1   | 338    | 1 LAMP_RAT   | Q62813 rattus norv |
| 25         | 92.5  | 5.1   | 340    | 1 BRA1_HUMAN | Q992v7 homo sapien |
| 26         | 92.5  | 5.1   | 4391   | 1 PGBM_HUMAN | P98160 homo sapien |
| 27         | 92    | 5.1   | 359    | 1 LACH_DROME | Q24372 drosophila  |
| 28         | 92    | 5.1   | 458    | 1 CD4_PANTR  | P16004 pan troglod |
| 29         | 92    | 5.1   | 461    | 1 STFI_BOVIN | Q04752 bos taurus  |
| 30         | 91.5  | 5.0   | 111    | 1 KV3E_MOUSE | P01657 mus musculu |
| 31         | 91.5  | 5.0   | 111    | 1 KV3J_MOUSE | P01662 mus musculu |
| 32         | 91.5  | 5.0   | 111    | 1 KV3K_MOUSE | P01663 mus musculu |
| 33         | 91.5  | 5.0   | 131    | 1 KV3I_MOUSE | P01661 mus musculu |

ALIGNMENTS

RESULT 1

DSCA\_HUMAN STANDARD; PRT; 2012 AA.

AC O60469; O60468;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Down syndrome cell adhesion molecule precursor (CHD2).

GN DSCAM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=Brain;

RX MEDLINE=98087574; PubMed=9426258;

RA Yamakawa K., Huot Y.-K., Haendelt M.A., Hubert R., Chen X.-N.,

RA Lyons G.E., Korenberg J.R.;

RT "DSCAM: a novel member of the immunoglobulin superfamily maps in a

RT Down syndrome region and is involved in the development of the

RT nervous system.";

RL Hum. Mol. Genet. 7:227-237(1998).

RN [2]

RP SEQUENCE FROM N.A., AND FUNCTION.

RX MEDLINE=20384934; PubMed=10925149;

RA Agarwala K.L., Nakamura S., Tsutsumi Y., Yamakawa K.;

RT "Down syndrome cell adhesion molecule DSCAM mediates homophilic

RT intercellular adhesion.";

RL Brain Res. Mol. Brain Res. 79:118-126(2000).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20289799; PubMed=10830953;

RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

RA Soeda E., Onki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

RA Minoshima S., Shimizu N., Nordieck G., Hornischer K., Brandt P.,

RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,

RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,

RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

RA Lehrach H., Reinhardt R., Yaspo M.-L.;

RT "The DNA sequence of human chromosome 21.";

RL Nature 405:311-319(2000).

CC -1- FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-

CC INDEPENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED IN

CC NERVOUS SYSTEM DEVELOPMENT.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE). THE

CC SHORT ISOFORM MAY BE SECRETED.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Long; Synonyms=CHD2-52;

CC IsoId=O60469-1; Sequence=Displayed;





QY 92 W-----TDRHVE-----EAQVW-----HWDROP-----PGVPH 115  
Db 157 WHLDGKPLVPNEKGVSKQETRRHPETGLTQLSELMTVPARGDPRPTFSCSFSGPLR 216  
QY 116 DRADRLDLYASGERRAYGFLDRVAV-----GADAFERGFSLRIE----- 159  
Db 217 HRALRTAPI-----QPRVWEPVPLEVQVVEPEGGAVERGGITVLTCEVPAQSPQIHW 272  
QY 160 ----PLEV-----ADEQTSCHLHHYCGCHERRVFLTVAEPAEPFPPRGS 202  
Db 273 KDGVPFLPSPSVLILPEIGPDQGTSCVATHSHGQESRAVSISIEPGEEGTAGS 332  
QY 203 PCNGSSHSGAGPDPTLARGHNVINIVPESRAHFFQQLGYVLTALLFI-----L 253  
Db 333 VG-----GSLGLTLALALGILGLGTAA 355  
QY 254 LLVTVLLAARRRRGGYEYDQKSGKSGKDVNLAE 288  
Db 356 LLIGVILWQRRORRGE-----RKAPENQEEERAE 387  
RESULT 3  
A33\_HUMAN STANDARD; PRT; 319 AA.  
AC Q99795;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 15-SEP-2003 (Rel. 42, last annotation update)  
DE Cell surface A33 antigen precursor (Glycoprotein A33).  
GN GPA33.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Colon carcinoma;  
RX MEDLINE=97165045; PubMed=9012807;  
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,  
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,  
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,  
RA Burgess A.W.;  
RT "The human A33 antigen is a transmembrane glycoprotein and a novel  
RT member of the immunoglobulin superfamily."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).  
RN [2]  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=97396159; PubMed=9245713;  
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,  
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,  
RA Simpson R.J.;  
RT "Characterization of posttranslational modifications of human A33  
RT antigen, a novel palmitoylated surface glycoprotein of human  
RT gastrointestinal epithelium."  
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).  
CC -!- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.  
CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL  
CC EPITHELIUM AND IN 95% OF COLON CANCERS.  
CC -!- PFM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED  
CC CARBOHYDRATE.  
CC -!- PFM: PALMITOYLATED.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
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CC -----

DR EMBL; U79725; AAC50957.1; -.  
DR Genew; HGNC:4445; GPA33.  
DR MIM; 602171; -.  
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;  
KW Transmembrane; Signal; Antigen.  
FT SIGNAL 1 21  
FT CHAIN 22 319 CELL SURFACE A33 ANTIGEN.  
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 236 256 POTENTIAL.  
FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 22 134 IG-LIKE V-TYPE.  
FT DOMAIN 140 227 IG-LIKE C2-TYPE.  
FT DOMAIN 258 261 POLY-CYS.  
FT DISULFID 43 117 POTENTIAL.  
FT DISULFID 146 222 POTENTIAL.  
FT DISULFID 162 211 POTENTIAL.  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;  
Query Match 6.0%; Score 108.5; DB 1; Length 319;  
Best Local Similarity 25.6%; Pred. No. 0.074;  
Matches 50; Conservative 33; Mismatches 79; Indels 33; Gaps 10;  
QY 45 LYESLAVRLEVTGPPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVW 104  
Db 9 LWTLCARVTVDAISVETP-----QDVLRAQSGKSVTLPCY--HTST-----SSREGLI 56  
QY 105 HMDRQPPGVPHDRADRLDLYASGERRAYGFLDRVAVGADAFERGFSLRIEPLVA 164  
Db 57 QWDK-----LLLTHTERVVWPFNSKNYHGYLY-KNRVVISNNA-EQSDASITIDQLTMA 110  
QY 165 DEGTYSK--HLHHYCGCHERRVFLTVAEPAEPFPPRGS PGNG-----SSHSGA 212  
Db 111 DNGTYECSVSLMSDLEGNTKSRVLLVLVPP--SKPEGIEGETIIGNNIQLTQCSKEGS 168  
QY 213 PGDPPTLARGHNVIN 227  
Db 169 PTFQYSWKR-YNILN 182  
RESULT 4  
CXAR\_HUMAN STANDARD; PRT; 365 AA.  
AC P78310; O00694;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, last sequence update)  
DT 15-SEP-2003 (Rel. 42, last annotation update)  
DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-  
DE adenovirus receptor) (hCAR) (CVB3 binding protein).  
GN CXADR OR CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97190109; PubMed=9036860;  
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;  
RT "Isolation of a common receptor for Cocksackie B viruses and  
RT adenoviruses 2 and 5."  
RL Science 275:1320-1323(1997).  
RN [2]





RP SEQUENCE FROM N.A.  
RA Hashimoto O., Tatsumi M.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE OF 28-424 FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=93049640; PubMed=1425921;  
RA Fomsgaard A., Hirsch V.M., Johnson P.R.;  
RT "Cloning and sequences of primate CD4 molecules: diversity of the  
RT cellular receptor for simian immunodeficiency virus/human  
RT immunodeficiency virus."  
RL Eur. J. Immunol. 22:2973-2981(1992).  
CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL  
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.  
CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
-----  
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-----  
CC EMBL; D63346; BAA09670.1; -  
CC EMBL; X73325; CAA51751.1; -  
CC HSP; P01730; IWER.  
DR GO; GO:0042101; C:T-cell receptor complex; ISS.  
DR GO; GO:0015026; P:coreceptor activity; ISS.  
DR GO; GO:0042289; P:MHC class II protein binding activity; ISS.  
DR GO; GO:0006955; P:immune response; ISS.  
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.  
DR GO; GO:0030217; P:T-cell differentiation; ISS.  
DR GO; GO:0045058; P:T-cell selection; ISS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.  
DR InterPro; IPR000973; CD4 TCRG.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_2.  
DR PRINTS; PR00692; CD4TCRANTIGEN.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;  
KW Immune response; Repeat; Signal; Lipoprotein; Palmitate.  
FT SIGNAL 1 25  
FT CHAIN 26 458  
FT DOMAIN 26 396  
FT TRANSMEM 397 418  
FT DOMAIN 419 458  
FT DOMAIN 26 125  
FT DOMAIN 126 203  
FT DOMAIN 204 317  
FT DOMAIN 318 374  
FT CARBOHYD 42 42  
FT CARBOHYD 296 296  
FT CARBOHYD 325 325  
FT DISULFID 41 109  
FT DISULFID 155 184  
FT DISULFID 328 370  
FT LIPID 419 419  
FT LIPID 422 422  
FT CONFLICT 57 57  
FT CONFLICT 91 91  
FT CONFLICT 105 105  
FT CONFLICT 113 113  
FT CONFLICT 302 302  
FT CONFLICT 349 349  
FT SEQUENCE 458 AA; 50905 MW; 751A9BA2C8B3EE16 CRC64;

Query Match 5.7%; Score 104; DB 1; Length 458;  
Best Local Similarity 22.7%; Pred. No. 0.28;  
Matches 59; Conservative 35; Mismatches 94; Indels 72; Gaps 12;  
QY 63 PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVQVHWDQPPGVPHDRADRL 122  
Db 20 PAVTQGGKVLG-KKGDVLTLC-----NASQKNTQFHW-----KNSDQIK 60  
QY 123 DLYASGERRAYGFLFLDRVAVGADAFERGFSLRLEPVEADGTYSCHLHHVCGLHE 182  
Db 61 ILGIQGSFLTCKPSKLSRADSRKSLWDQGCFSMIKNLKIEDSNTYICEVENEKEEV-E 119  
QY 183 RRVFHLTV-AEPH-----AEPFPPRGSPGNGSHSGAPGPDPTLARGHNVINVIP 231  
Db 120 LLVFGLTANSDTHLLEGQSLTLTLESPPGSSP---SVKCRSPG-----GKNI----- 163  
QY 232 ESRAHFFQOLGYVLTATLLFILLVTVLLAARRRRGGYEYS---DQSKGSKGKDVNLAE 288  
Db 164 -----QGGRTLSVPQL-----ERQDSCTWCTVSDQKTVEFK---IDIVV 201  
QY 289 FAVAAGDQMLYRSEDILQDY 308  
Db 202 LAFQKASSTVYKKEGEQVEF 221

## RESULT 6

## LAG3\_HUMAN

ID LAG3\_HUMAN STANDARD; PRT; 525 AA.  
AC P18627;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 28-FEB-2003 (Rel. 41, last sequence update)  
DE 15-SEP-2003 (Rel. 42, last annotation update)  
DE Lymphocyte activation gene-3 protein precursor (LAG-3) (FDC protein)  
DE (CD223 antigen).  
GN LAG3 OR FDC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90237736; PubMed=1692078;  
RA Triebel F., Jitsukawa S., Baixeras E., Roman-Roman S., Genevee C.,  
RA Viegas-Pequignot E., Hercend T.;  
RT "LAG-3, a novel lymphocyte activation gene closely related to CD4."  
RL J. Exp. Med. 171:1393-1405(1990).  
RN [2]  
RP REVISIONS TO C-TERMINUS.  
RA Triebel F.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=92364535; PubMed=1380059;  
RA Baixeras E., Huard B., Miossec C., Jitsukawa S., Martin M.,  
RA Hercend T., Auffray C., Triebel F., Piatier-Tonneau D.;  
RT "Characterization of the lymphocyte activation gene 3-encoded  
RT protein. A new ligand for human leukocyte antigen class II  
RT antigens."  
RL J. Exp. Med. 176:327-337(1992).  
CC -!- FUNCTION: INVOLVED IN LYMPHOCYTE ACTIVATION. BINDS TO HLA CLASS-II  
CC ANTIGENS.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: ON CELL SURFACE OF ACTIVATED NK AND  
CC T-LYMPHOCYTES.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -!- DATABASE: NAME=PROW; NOTE=PROW 3:15-18(2002);  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1656481751.g.htm".  
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EMBL; X51985; CAA36243.3; -  
 EMBL; A21353; CAA01547.1; ALT\_SEQ.  
 Genew; HGNC:6476; LAG3.  
 MIM; 153337; -  
 GO; GO:0003823; F:antigen binding activity; TAS.  
 InterPro; IPR007110; Ig-like.  
 InterPro; IPR003599; Ig.  
 InterPro; IPR003006; Ig\_MHC.  
 Pfam; PF00047; Ig; 3.  
 SMART; SM00409; Ig; 3.  
 PROSITE; PS50835; IG\_LIKE; 2.  
 Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.  
 SIGNAL 1 28  
 CHAIN 29 525 LYMPOCYTE ACTIVATION GENE-3 PROTEIN.  
 DOMAIN 29 450 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 451 471 POTENTIAL.  
 DOMAIN 472 525 CYTOPLASMIC (POTENTIAL).  
 DOMAIN 37 167 IG-LIKE V-TYPE.  
 DOMAIN 168 252 IG-LIKE C2-TYPE 1.  
 DOMAIN 265 343 IG-LIKE C2-TYPE 2.  
 DOMAIN 348 419 IG-LIKE C2-TYPE 3.  
 DISULFID 44 160 POTENTIAL.  
 DISULFID 189 241 POTENTIAL.  
 DISULFID 282 333 POTENTIAL.  
 DISULFID 369 412 POTENTIAL.  
 CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).  
 CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SEQUENCE 525 AA; 57436 MW; C711EDB0E9E2733 CRC64;

Query Match 5.5%; Score 100.5; DB 1; Length 525;  
 Best Local Similarity 26.6%; Pred. No. 0.65;  
 Matches 46; Conservative 9; Mismatches 69; Indels 49; Gaps 5;  
 QY 60 PATPAYWDGEKVLAVARGAPALLTC-----VNRGHVWTDHVEEAQQVWHD 108  
 Db 19 PVKPLQPGAEPVVMQAQGAQAPLPCSPPIQLDLSLRAG-----VTWQH 65  
 QY 109 QP-----PGV-----PHDRADRLLDLYASGERRAYGFLRDRVAVG 145  
 Db 66 QPDSGPPAAAGPHPLAGPHPAAPSSWGPRPRRTVLSVGPGLRS--GRPLQPRVQLD 123  
 QY 146 ADAFERGDFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHAEP 198  
 Db 124 ERGRQGRGDFSLWLRPARRADAGEYRAAVHLRDLRSLRLRLGQASMTASPP 176

RESULT 7  
 Y497\_MYCTU STANDARD; PRT; 310 AA.  
 AC Q11162;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein RV0497.  
 GN RV0497 OR MT0517 OR MTCY20G9.23.  
 OS Mycobacterium tuberculosis  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37Rv;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jgels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: TO M.LEPRAE ML2433.  
 CC -----  
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RESULT 8  
 JAM1\_MOUSE  
 ID JAM1\_MOUSE STANDARD; PRT; 300 AA.  
 AC O88792;  
 DT 16-OCT-2001 (Rel. 40, Created)



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CC -----  
CC EMBL; X12752; CAA31242.1; -  
CC PIR; S06890; A54265.  
CC TRANSFAC; T00108; -  
CC InterPro; IPR004827; TF\_bZIP.  
CC Pfam; PF00170; bZIP; 1.  
CC SMART; SM00338; BRLZ; 1.  
CC PROSITE; PS0217; bZIP; 1.  
CC PROSITE; PS00036; bZIP\_BASIC; FALSE\_NEG.  
CC Transcription regulation; Activator; DNA-binding; Nuclear protein.  
CC FT DOMAIN 181 190 POLY-PRO.  
CC FT DOMAIN 262 272 POLY-GLY.  
CC FT DNA BIND 286 306 BASIC MOTIF.  
CC FT DOMAIN 317 345 LEUCINE-ZIPPER.  
CC SQ SEQUENCE 358 AA; 37371 MW; 4DA8F112F6EA95D0 CRC64;

Query Match 5.4%; Score 98; DB 1; Length 358;  
Best Local Similarity 24.2%; Pred. No. 0.66;  
Matches 46; Conservative 9; Mismatches 59; Indels 76; Gaps 8;  
QY 58 GPP-----ATPAYWGEKEVLAVARGAPALLTCVNRGHVWTDHVEAQQVV-----HW 106  
Db 124 GPPGCGYCAAGYLDGRLEPLVERVGPALRPLVIKQE---PREDEAKQLALAGLFPYQ 180  
QY 107 DRQPGVPHDRADRLLDLYASGERRAYGFLRDRVAVGADAFERGFSLRLEPLEVADE 166  
Db 181 PPPPPPPPPHFA-----SPAHLA-- 198  
QY 167 GTYSCHLHH--YCGLHERRVFLTVAEPHAEPPP-----RGSPGNGSSHSGA 212  
Db 199 ---APHLQFIARCG---QTTMLQPGHPTPTTPVSPHPAPAMGAAGLPGPGSLKGL 252  
QY 213 PGPDPTLARG 222  
Db 253 AGHPDPLRTG 262

RESULT 10  
P53\_MARMO STANDARD; PRT; 391 AA.  
AC Q36006;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53.  
OS Marmota monax (Woodchuck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;  
OC Marmota.  
OX NCBI\_TaxID=9995;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97376996; PubMed=9233767;  
RA Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;  
RT "Partial characterization of the woodchuck tumor suppressor, p53, and  
RT its interaction with woodchuck hepatitis virus X antigen in  
RT hepatocarcinogenesis."  
RL Oncogene 15:327-336(1997).  
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of

CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: p53 is found in increased amounts in a wide variety  
CC of transformed cells. p53 is frequently mutated or inactivated  
CC in many types of cancer.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC -----  
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CC -----  
CC EMBL; AJ001022; CAA04478.1; -  
CC HSSP; P04637; ITUP.  
CC InterPro; IPR002117; P53.  
CC Pfam; PF00870; P53; 1.  
CC PRINTS; PR00386; P53SUPPRESSR.  
CC PRODOM; PD002681; P53; 1.  
CC PROSITE; PS00348; P53; 1.  
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
CC Nuclear protein; Phosphorylation; Apoptosis.  
CC FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
CC FT DNA BIND 100 290 BY SIMILARITY.  
CC FT DOMAIN 323 354 OLIGOMERIZATION.  
CC FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).  
CC FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
CC FT MOD\_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY  
CC SIMILARITY).  
CC FT MOD\_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).  
CC SQ SEQUENCE 391 AA; 43468 MW; E1DE5B84BA40182 CRC64;

Query Match 5.3%; Score 97; DB 1; Length 391;  
Best Local Similarity 21.5%; Pred. No. 0.89;  
Matches 67; Conservative 33; Mismatches 101; Indels 110; Gaps 14;  
QY 1 MALPSRILLKLVLLQSSAV-----LLHSAVBETDAGLYTCNLHHHYCHL 45  
Db 80 LAAPSPATSWPL-----SSVPSQNTYPGVYGRGLHSGTAKSVTCTYSPSLNKLFCQL 135  
QY 46 YESLAVRLEVTGDP-----ATPAYWGEKEVLAVARGAPALLTCVNRGHVWTDHVEEA 100  
Db 136 AKTCPVLWVDSTPPPGTRVRAAIYKKSQHTMTEVVRCPHERCSDSLAPPQHL--- 192  
QY 101 QQVHWDRQPGVPHDRADRLLDLYASGERRAYGFLRDRVAVGADAFERGFSLRIEP 160  
Db 193 -----IRVEGNLRAE---YLDDR-----NTF-RHSVVVPYEP 220  
QY 161 LEVADEGTYSCHLHHY-----C-GLHERRV-----FHLT----- 190  
Db 221 PEVGSSECT---TIHYNMNCSSCGMNRRLPILITITLEGSSGNLLGRNSFEVRVCACPG 277  
QY 191 -----AEPHAEPPIPRGSP---GNGSSHSGAPGPDPTLARGHNVINIVPESR 234  
Db 278 RDRRTTEENFRKRGEPCEPPPRSTKRALPNGTSSSPQPKKP--LDGEYFTLKIRGRAR 335  
QY 235 AHFFQQLGYVL 245  
Db 336 FEMFQELNEAL 346

RESULT 11  
CD4\_MACFA STANDARD; PRT; 458 AA.  
ID CD4\_MACFA  
AC P79185;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen





FT CHAIN 26 458 T-CELL SURFACE GLYCOPROTEIN CD4.  
FT DOMAIN 26 396 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 397 418 POTENTIAL.  
FT DOMAIN 419 458 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 26 125 IG-LIKE V-TYPE.  
FT DOMAIN 126 203 IG-LIKE C2-TYPE 1.  
FT DOMAIN 204 317 IG-LIKE C2-TYPE 2.  
FT DOMAIN 318 374 IG-LIKE C2-TYPE 3.  
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (BY SIMILARITY).  
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (BY SIMILARITY).  
FT DISULFID 41 109 BY SIMILARITY.  
FT DISULFID 155 184 BY SIMILARITY.  
FT DISULFID 328 370 BY SIMILARITY.  
FT LIPID 419 419 PALMITATE (BY SIMILARITY).  
FT LIPID 422 422 PALMITATE (BY SIMILARITY).  
SQ SEQUENCE 458 AA; 50828 MW; 76B3E7EF08185535 CRC64;

Query Match 5.3%; Score 97; DB 1; Length 458;  
Best Local Similarity 21.9%; Pred. No. 1.1;  
Matches 57; Conservative 35; Mismatches 96; Indels 72; Gaps 12;

QY 63 PAYWDEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHVWDROPVGVPHDRDLRL 122  
Db PAVTQCKKVLG-KKGDIVELTC-----NASQKNTQFHW-----KNSNQIK 60

QY 123 DLYAGERRAYGFLFDRVAVGADAFERGFDSRIEPLVADGTYSCHLHHYCGLHE 182  
Db 61 ILGIQGSFLTQKPSKLSDRADSRKSLWDQCFSMIKNTKIEDSDTYICEVENKKEV-E 119

QY 183 RRVFHLTV-AEPH-----AEPHPRGSPGNSHSGAPGDPPLARGHNV---INV 228  
Db 120 LLVFLGTANSDFHLEQSLTLESPGSSP---SVKCRSPG-----GKNIQGGRTI 169

QY 229 IVPESRAHFFQOLGYVLTLLPILLVTVLLAARRRRGGYEYSDDKSGKSGKDVNLAE 288  
Db 170 SVPQLER---QDSGTWTCTV-----SQDKTVEFK---IDIVV 201

QY 289 FAVAAGDQMLYRSEDIDLXY 308  
Db 202 LAFQKASSTVYKGEQVEF 221

RESULT 13  
PTK7\_HUMAN  
ID PTK7\_HUMAN STANDARD; PRT; 1070 AA.  
AC Q13308; Q13417;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)  
DE (CCK-4).  
GN PTK7 OR CCK4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon carcinoma, and Placenta;  
RX MEDLINE=96074849; PubMed=7478540;  
RA Mossie K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A.;  
RT "Colon carcinoma kinase-4 defines a new subclass of the receptor  
RT tyrosine kinase family."  
RL Oncogene 11:2179-2184(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=97037064; PubMed=8882711;  
RA Park S.-K., Lee H.-S., Lee S.-T.;  
RT "Characterization of the human full-length PTK7 cDNA encoding a  
RT receptor protein tyrosine kinase-like molecule closely related to  
RT chick KLG."

RL J. Biochem. 119:235-239(1996).  
RN [3]  
RP SEQUENCE FROM N.A., AND REVISION TO 834.  
RA Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY  
CC THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE  
CC PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR  
CC PROGRESSION MARKER.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,  
CC KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID  
CC GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN  
CC ERYTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN  
CC RECEPTOR SUBFAMILY.  
CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
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CC -----  
DR EMBL; U33635; AAA87565.1; -  
DR EMBL; U40271; AAC50484.2; -  
DR EMBL; AF447176; AAL39062.1; -  
DR EMBL; AF447157; AAL39062.1; JOINED.  
DR EMBL; AF447158; AAL39062.1; JOINED.  
DR EMBL; AF447162; AAL39062.1; JOINED.  
DR EMBL; AF447164; AAL39062.1; JOINED.  
DR EMBL; AF447167; AAL39062.1; JOINED.  
DR EMBL; AF447170; AAL39062.1; JOINED.  
DR EMBL; AF447171; AAL39062.1; JOINED.  
DR EMBL; AF447173; AAL39062.1; JOINED.  
DR EMBL; AF447174; AAL39062.1; JOINED.  
DR EMBL; AF447175; AAL39062.1; JOINED.  
DR HSSP; P08631; 1AD5.  
DR Genew; HGNC:9618; PTK7.  
DR MIM; 601890; -  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.  
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002011; RTKinaseII.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00047; ig; 7.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00408; IGC2; 5.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00835; IG LIKE; 7.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00239; RECEPTOR TYR KIN II; FALSE NEG.  
KW Receptor; Transmembrane; signal; Glycoprotein; Cell adhesion;  
KW Immunoglobulin domain; Repeat.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 1070 TYROSINE-PROTEIN KINASE-LIKE 7.  
FT DOMAIN 31 704 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 705 725 POTENTIAL.  
FT DOMAIN 726 1070 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 31 120 IG-LIKE C2-TYPE 1.  
FT DOMAIN 128 218 IG-LIKE C2-TYPE 2.  
FT DOMAIN 225 317 IG-LIKE C2-TYPE 3.  
FT DOMAIN 309 407 IG-LIKE C2-TYPE 4.





FT DOMAIN 123 175 PRO-RICH.  
FT DISULFID 43 110 POTENTIAL.  
FT DISULFID 57 65 POTENTIAL.  
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 224 AA; 24830 MW; 60C88716D84600D2 CRC64;  
  
Query Match 5.3%; Score 96; DB 1; Length 224;  
Best Local Similarity 26.6%; Pred. No. 0.54;  
Matches 50; Conservative 26; Mismatches 80; Indels 32; Gaps 11;  
  
QY 106 WDROPGVPHDRLLDLVSGERRAYGFLFDRDRAVAGDAFERGDFSLRIEPLVAD 165  
Db 56 WCR-PPQIL--RCDKIVETKSGAKR-NGRVSIRDSPA-----NLSFTVTLENLTED 104  
  
QY 166 EGTYSCHLHHYCGLHE--RRVPHLTVAEPHAEPPRPGSPGNGSSHS--GAPGPDPTLAR 221  
Db 105 AGTY-----WCGVDPWLRDFHDPIVEVEVSVPAGTTASSPOSSMGTSGP-PTKLP 156  
  
QY 222 GH---NVINVIVPESRAH---FPQQLGYVLATLL--LFILLVTVLLAARRRRGGVEYS 272  
Db 157 VHTWPSVTRKDSPEPSPHPGSLFSNVRELLLVLELPLLLMLGAVLWVNRQSRSSRQ 216  
  
QY 273 DQSGKSK 280  
Db 217 NWPKGENQ 224

## RESULT 15

CD8B HUMAN  
ID CD8B HUMAN STANDARD; PRT; 210 AA.  
AC P10966; P14861; Q9UQ55;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE T-cell surface glycoprotein CD8 beta chain precursor (Antigen CD8B).  
GN CD8B1 OR CD8B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=T-cell;  
RX MEDLINE=89091085; PubMed=3145195;  
RA Norment A.M., Littman D.R.;  
RT "A second subunit of CD8 is expressed in human T cells.";  
RL EMBO J. 7:3433-3439(1988).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=89091089; PubMed=3145196;  
RA Disanto J.P., Knowles R.W., Flomenberg N.;  
RT "The human LYT-3 molecule requires CD8 for cell surface expression.";  
RL EMBO J. 7:3465-3470(1988).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=89067811; PubMed=3264320;  
RA Shue L., Gorman S.D., Parnes J.R.;  
RT "A second chain of human CD8 is expressed on peripheral blood lymphocytes.";  
RL J. Exp. Med. 168:1993-2005(1988).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
RX MEDLINE=92176658; PubMed=1541829;  
RA Nakayama K., Kawachi Y., Tokito S., Minami N., Yamamoto R.,  
RA Imai T., Gachelin G., Nakauchi H.;  
RT "Recent duplication of the two human CD8 beta-chain genes.";  
RL J. Immunol. 148:1919-1927(1992).  
CC -!- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN THE PROCESS OF T-CELL MEDIATED KILLING.  
CC -!- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN LINKED BY TWO DISULFIDE BONDS.  
  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM 3 SEEMS TO BE SECRETED.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=M-1;  
CC IsoId=P10966-1; Sequence=Displayed;  
CC Name=2; Synonyms=M-3;  
CC IsoId=P10966-2; Sequence=VSP\_002490;  
CC Name=3; Synonyms=S-1;  
CC IsoId=P10966-3; Sequence=VSP\_002492, VSP\_002493;  
CC Name=4; Synonyms=M-2;  
CC IsoId=P10966-4; Sequence=VSP\_002491;  
CC -!- PTM: PHOSPHORYLATED AS A CONSEQUENCE OF T-CELL ACTIVATION (POSSIBLE).  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD8b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd8beta.htm".  
  
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CC -----  
CC EMBL; X13444; CAA31795.1; -  
CC EMBL; X13445; CAA31796.1; -  
CC EMBL; X13446; CAA31797.1; -  
CC EMBL; X13452; CAA31803.1; -  
CC EMBL; Y00805; CAA68750.1; -  
CC EMBL; M36712; AAA35864.1; -  
CC EMBL; S87090; AAB21669.2; -  
CC EMBL; S87068; AAB21669.2; JOINED.  
CC EMBL; S87070; AAB21669.2; JOINED.  
CC EMBL; S87073; AAB21669.2; JOINED.  
CC EMBL; S87081; AAB21669.2; JOINED.  
CC EMBL; S87087; AAB21670.2; -  
CC EMBL; S87068; AAB21670.2; JOINED.  
CC EMBL; S87070; AAB21670.2; JOINED.  
CC EMBL; S87073; AAB21670.2; JOINED.  
CC EMBL; S87078; AAB21670.2; JOINED.  
CC EMBL; S87081; AAB21670.2; JOINED.  
CC EMBL; S87083; AAB21671.2; -  
CC EMBL; S87068; AAB21671.2; JOINED.  
CC EMBL; S87070; AAB21671.2; JOINED.  
CC EMBL; S87073; AAB21671.2; JOINED.  
CC EMBL; S87078; AAB21671.2; JOINED.  
CC EMBL; S87081; AAB21671.2; JOINED.  
CC EMBL; S87083; AAB21672.2; -  
CC EMBL; S87068; AAB21672.2; JOINED.  
CC EMBL; S87070; AAB21672.2; JOINED.  
CC EMBL; S87073; AAB21672.2; JOINED.  
CC EMBL; S87078; AAB21672.2; JOINED.  
CC EMBL; S87081; AAB21672.2; JOINED.  
CC PIR; S01647; E46482.  
CC PIR; S01873; C46482.  
CC PIR; S01874; B46482.  
CC PIR; T01073; T01073.  
CC Genew; HGNC:1707; CD8B1.  
CC MIM; 186730; -  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0042101; C:T-cell receptor complex; NAS.  
CC GO; GO:0015026; F:coreceptor activity; NAS.  
CC GO; GO:0042288; F:MHC class I protein binding activity; NAS.  
CC GO; GO:0005515; F:protein binding activity; IPI.  
CC GO; GO:0006955; P:immune response; NAS.  
CC GO; GO:0042110; P:T-cell activation; NAS.  
CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003599; Ig.  
CC InterPro; IPR003006; Ig\_MHC.  
CC Pfam; PF00047; Ig; 1.



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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds

(without alignments)

1230.131 Million cell updates/sec

Title: US-10-006-818a-77

Perfect score: 1816

Sequence: 1 MALPSRILLWKLVLQSSAV.....SPLPAKYIDLDKGRKENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq 19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
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16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match | Length | ID          | Description        |
|------------|--------|-------|--------|-------------|--------------------|
| 1          | 1816   | 100.0 | 341    | 21 AAB24031 | Human PRO1293 prot |
| 2          | 1816   | 100.0 | 341    | 21 AAY99362 | Human PRO1293 (UNQ |
| 3          | 1816   | 100.0 | 341    | 22 AAB66111 | Protein of the inv |
| 4          | 1755.5 | 96.7  | 442    | 22 AAE06578 | Human protein havi |
| 5          | 1755.5 | 96.7  | 442    | 24 ABB84652 | Human SECP-4 prote |
| 6          | 1706   | 93.9  | 384    | 21 AAB36107 | Human MTC48. Homo  |
| 7          | 1694.5 | 93.3  | 450    | 22 AAB92464 | Human protein sequ |
| 8          | 1367.5 | 75.3  | 442    | 23 ABB72335 | Rat protein isolat |
| 9          | 1362.5 | 75.0  | 442    | 22 AAB85860 | Murine adipocytes- |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 1300  | 71.6 | 269 | 22 | ABB10350 | Human cDNA SEQ ID  |
| 11 | 1300  | 71.6 | 269 | 23 | ABP66937 | Human polypeptide  |
| 12 | 1006  | 55.4 | 290 | 21 | AAB59011 | Breast and ovarian |
| 13 | 955   | 52.6 | 192 | 22 | ABB10523 | Human cDNA SEQ ID  |
| 14 | 955   | 52.6 | 192 | 22 | AAU18028 | Human immunoglobul |
| 15 | 955   | 52.6 | 192 | 23 | ABP67110 | Human polypeptide  |
| 16 | 840   | 46.3 | 255 | 23 | ABB72366 | Murine protein iso |
| 17 | 826.5 | 45.5 | 260 | 21 | AAB36108 | Mouse MTC48. Mus   |
| 18 | 355   | 19.5 | 218 | 24 | ABB84671 | Human SECP-23 prot |
| 19 | 127   | 7.0  | 447 | 24 | ABR39440 | Human GENSET polyp |
| 20 | 125.5 | 6.9  | 651 | 19 | AAW62782 | Protein encoded by |
| 21 | 125   | 6.9  | 244 | 22 | AAB46060 | Human TF anti-idio |
| 22 | 123   | 6.8  | 650 | 19 | AAW82544 | Human LIR-P3G2 pro |
| 23 | 123   | 6.8  | 650 | 21 | AAB04169 | Leukocyte immunogl |
| 24 | 122   | 6.7  | 253 | 23 | ABP45328 | Human Blys binding |
| 25 | 122   | 6.7  | 652 | 19 | AAW82545 | Human LIR-18A3 pro |
| 26 | 122   | 6.7  | 652 | 21 | AAB04170 | Leukocyte immunogl |
| 27 | 121   | 6.7  | 254 | 23 | ABP45955 | Human Blys binding |
| 28 | 120   | 6.6  | 266 | 23 | ABG97835 | Single chain antib |
| 29 | 120   | 6.6  | 266 | 23 | ABG35336 | Thrombopoietin ago |
| 30 | 119.5 | 6.6  | 246 | 21 | AAV15126 | Anti-murine CTLA-4 |
| 31 | 119.5 | 6.6  | 249 | 23 | ABP45951 | Human Blys binding |
| 32 | 119   | 6.6  | 240 | 22 | AAB46058 | Human TF anti-idio |
| 33 | 118.5 | 6.5  | 448 | 19 | AAW82551 | Human LIR-pbm2 pro |
| 34 | 118.5 | 6.5  | 448 | 19 | AAW53463 | Human gp49 HM18 po |
| 35 | 118.5 | 6.5  | 448 | 21 | AAB04176 | Leukocyte immunogl |
| 36 | 118.5 | 6.5  | 469 | 22 | AAW41582 | Human polypeptide  |
| 37 | 117.5 | 6.5  | 472 | 19 | AAW69234 | FCR-IV protein seq |
| 38 | 117   | 6.4  | 239 | 22 | AAB46059 | Human TF anti-idio |
| 39 | 116.5 | 6.4  | 328 | 23 | AAO19049 | Antibody 12B10 sin |
| 40 | 116.5 | 6.4  | 328 | 23 | AAO19049 | Cell adhesion mole |
| 41 | 116   | 6.4  | 253 | 23 | ABP45591 | Human Blys binding |
| 42 | 115.5 | 6.4  | 249 | 23 | ABP45607 | Human Blys binding |
| 43 | 115.5 | 6.4  | 251 | 23 | ABP45535 | Human Blys binding |
| 44 | 115.5 | 6.4  | 533 | 22 | AAW93372 | Human polypeptide, |
| 45 | 115.5 | 6.4  | 534 | 22 | AAU00906 | Human B lymphocyte |

ALIGNMENTS

RESULT 1

AAB24031  
ID AAB24031 standard; Protein; 341 AA.  
XX AAB24031;  
AC AAB24031;  
XX 25-JAN-2001 (first entry)  
DT Human PRO1293 protein sequence SEQ ID NO:31.  
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
KW identification; tumourigenesis; anticancer; detection.  
XX Homo sapiens.  
OS  
XX  
XX WO200053750-A1.  
XX  
XX 14-SEP-2000  
XX  
XX 02-DEC-1999; 99WO-US28551.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
XX  
XX 01-SEP-1999; 99WO-US20111.  
XX  
XX 29-OCT-1999; 99US-0162506.  
XX  
XX 30-NOV-1999; 99WO-US28313.  
XX  
XX 01-DEC-1999; 99WO-US28634.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
XX  
XX WPI; 2000-594320/56.

Sequence 'A'

See over

sequence, A,

|          |  |  |
|----------|--|--|
| DR       | N-PSDB; AAC58113.  |  |
| XX       | Antibodies specific for PRO polypeptides, used to diagnose and inhibit   |  |
| PT       | the growth of tumors in mammals, and to identify inhibitors of PRO       |  |
| PT       | polypeptide activity or expression -                                     |  |
| XX       | Claim 61; Fig 22; 226pp; English.  |  |
| PS       |  |  |
| XX       | The present invention describes an antibody that binds to a human        |  |
| CC       | protein (I) selected from: PRO1269; PRO1410; PRO1755; PRO1780;           |  |
| CC       | PRO3434; PRO1927; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354;           |  |
| CC       | PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has        |  |
| CC       | anticancer activity and can be used to diagnose tumours in mammals, by   |  |
| CC       | detecting complex formation when the antibody is contacted with test     |  |
| CC       | cells. Increased expression of genes encoding (I) can also be detected   |  |
| CC       | to diagnose tumours. Agents which inhibit the activity of (I),           |  |
| CC       | especially the antibodies, or an antisense oligonucleotide which         |  |
| CC       | hybridises to genes encoding (I), can be used to inhibit tumour growth,  |  |
| CC       | preferably by inducing cell death. Methods from the present invention    |  |
| CC       | can be used to identify compounds which inhibit the biological activity  |  |
| CC       | of (I). AAC58109 to AAC58102 represent PCR primers and hybridisation     |  |
| CC       | probes used in examples from the present invention for human PRO         |  |
| CC       | sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human |  |
| CC       | PRO polynucleotide and protein sequences given in the exemplification of |  |
| CC       | the present invention.   |  |
| XX       |  |  |
| SQ       | Sequence 341 AA;   |  |
|          | Query Match 100.0%; Score 1816; DB 21; Length 341;                       |  |
|          | Best Local Similarity 100.0%; Pred. No. 4.8e-155;                        |  |
|          | Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;             |  |
| Qy       | 1 MALPSRILLKVLQSSAVLLHSAVEETDAGLYTCNLRHHYCHLYESLAVRLEVTGPP 60            |  |
| Db       | 1 MALPSRILLKVLQSSAVLLHSAVEETDAGLYTCNLRHHYCHLYESLAVRLEVTGPP 60            |  |
| Qy       | 61 ATPAYWDEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVWVHWRQPPGVPHDRADR 120         |  |
| Db       | 61 ATPAYWDEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVWVHWRQPPGVPHDRADR 120         |  |
| Qy       | 121 LLDLYASGERRAYGFLFDRVAVGADAFERGFDSLRLEPLEVADEGTYSCHLHHYCG 180         |  |
| Db       | 121 LLDLYASGERRAYGFLFDRVAVGADAFERGFDSLRLEPLEVADEGTYSCHLHHYCG 180         |  |
| Qy       | 181 HERRVFLTVAEPHAEPGRGSPGNGSSHSAGPDPPTLARGHNVINVTVPESRAHFFQ 240         |  |
| Db       | 181 HERRVFLTVAEPHAEPGRGSPGNGSSHSAGPDPPTLARGHNVINVTVPESRAHFFQ 240         |  |
| Qy       | 241 LGYVLATLLLFILLVTVLLAARRRGGEYSDQSKSGKGVNLAFAVAAGDQMLYR 300            |  |
| Db       | 241 LGYVLATLLLFILLVTVLLAARRRGGEYSDQSKSGKGVNLAFAVAAGDQMLYR 300            |  |
| Qy       | 301 SEDIQLDYKNNILKERAELAHSPAKYIDLDKGRKENCK 341                           |  |
| Db       | 301 SEDIQLDYKNNILKERAELAHSPAKYIDLDKGRKENCK 341                           |  |
| RESULT 2 |  |  |
| AY99362  |  |  |
| ID       | AY99362 standard; Protein; 341 AA.                                       |  |
| XX       |  |  |
| AC       | AY99362;   |  |
| XX       |  |  |
| DT       | 08-AUG-2000 (first entry)  |  |
| XX       |  |  |
| DE       | Human PRO1293 (UNQ662) amino acid sequence SEQ ID NO:77.                 |  |
| XX       |  |  |
| KW       | Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;     |  |
| KW       | transmembrane; secretion; immunoadhesion; pharmaceutical; screening.     |  |
| XX       |  |  |
| OS       | Homo sapiens.  |  |
| XX       |  |  |
| PN       | WO200012708-A2.  |  |

|    |              |               |
|----|--------------|---------------|
| XX | 09-MAR-2000. |               |
| PD |              |               |
| XX |              |               |
| PF | 01-SEP-1999; | 99WO-US20111. |
| XX |              |               |
| PR | 01-SEP-1998; | 98US-0098716. |
| PR | 01-SEP-1998; | 98US-0098749. |
| PR | 02-SEP-1998; | 98US-0098750. |
| PR | 02-SEP-1998; | 98US-0098803. |
| PR | 02-SEP-1998; | 98US-0098821. |
| PR | 02-SEP-1998; | 98US-0098843. |
| PR | 09-SEP-1998; | 98US-0099536. |
| PR | 09-SEP-1998; | 98US-0099596. |
| PR | 09-SEP-1998; | 98US-0099598. |
| PR | 09-SEP-1998; | 98US-0099602. |
| PR | 09-SEP-1998; | 98US-0099642. |
| PR | 10-SEP-1998; | 98US-0099741. |
| PR | 10-SEP-1998; | 98US-0099754. |
| PR | 10-SEP-1998; | 98US-0099763. |
| PR | 10-SEP-1998; | 98US-0099792. |
| PR | 10-SEP-1998; | 98US-0099808. |
| PR | 10-SEP-1998; | 98US-0099812. |
| PR | 10-SEP-1998; | 98US-0099815. |
| PR | 15-SEP-1998; | 98US-0099816. |
| PR | 15-SEP-1998; | 98US-0100385. |
| PR | 15-SEP-1998; | 98US-0100388. |
| PR | 15-SEP-1998; | 98US-0100390. |
| PR | 16-SEP-1998; | 98US-0100584. |
| PR | 16-SEP-1998; | 98US-0100627. |
| PR | 16-SEP-1998; | 98US-0100661. |
| PR | 16-SEP-1998; | 98US-0100662. |
| PR | 16-SEP-1998; | 98US-0100664. |
| PR | 17-SEP-1998; | 98US-0100683. |
| PR | 17-SEP-1998; | 98US-0100684. |
| PR | 17-SEP-1998; | 98US-0100710. |
| PR | 17-SEP-1998; | 98US-0100711. |
| PR | 17-SEP-1998; | 98US-0100919. |
| PR | 17-SEP-1998; | 98US-0100930. |
| PR | 18-SEP-1998; | 98US-0100848. |
| PR | 18-SEP-1998; | 98US-0100849. |
| PR | 18-SEP-1998; | 98US-0101014. |
| PR | 18-SEP-1998; | 98US-0101068. |
| PR | 22-SEP-1998; | 98US-0101071. |
| PR | 22-SEP-1998; | 98US-0101279. |
| PR | 23-SEP-1998; | 98US-0101471. |
| PR | 23-SEP-1998; | 98US-0101472. |
| PR | 23-SEP-1998; | 98US-0101474. |
| PR | 23-SEP-1998; | 98US-0101475. |
| PR | 23-SEP-1998; | 98US-0101476. |
| PR | 23-SEP-1998; | 98US-0101477. |
| PR | 23-SEP-1998; | 98US-0101479. |
| PR | 24-SEP-1998; | 98US-0101738. |
| PR | 24-SEP-1998; | 98US-0101741. |
| PR | 24-SEP-1998; | 98US-0101743. |
| PR | 24-SEP-1998; | 98US-0101915. |
| PR | 24-SEP-1998; | 98US-0101916. |
| PR | 29-SEP-1998; | 98US-0102207. |
| PR | 29-SEP-1998; | 98US-0102240. |
| PR | 29-SEP-1998; | 98US-0102307. |
| PR | 29-SEP-1998; | 98US-0102330. |
| PR | 30-SEP-1998; | 98US-0102331. |
| PR | 30-SEP-1998; | 98US-0102484. |
| PR | 30-SEP-1998; | 98US-0102487. |
| PR | 30-SEP-1998; | 98US-0102570. |
| PR | 30-SEP-1998; | 98US-0102571. |
| PR | 01-OCT-1998; | 98US-0102684. |
| PR | 01-OCT-1998; | 98US-0102687. |
| PR | 02-OCT-1998; | 98US-0102965. |
| PR | 06-OCT-1998; | 98US-0103258. |
| PR | 06-OCT-1998; | 98US-0103449. |
| PR | 07-OCT-1998; | 98US-0103314. |
| PR | 07-OCT-1998; | 98US-0103315. |
| PR | 07-OCT-1998; | 98US-0103328. |

Sequence, Comparison

|    |   |  |
|----|---|--|
| DR | N-PSDB; AAC58113.   |  |
| XX | Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression -  |  |
| PT | Claim 61; Fig 22; 226pp; English.   |  |
| XX | The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO1927; PRO3567; PRO1295; PRO1293; PRO3303; PRO4344; PRO4354; PRO4397; PRO4407; PRO1555; PRO10596; PRO2038; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention. |  |
| XX | Sequence 341 AA;  |  |
| SQ | Query Match 100.0%; Score 1816; DB 21; Length 341; Best Local Similarity 100.0%; Pred. No. 4.8e-155; Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |  |
| Qy | 1 MALPSRILLKLVLLQSSAVLLHSAVEETDAGLYTCNLLHHYCHLYESLAVLEVTGPP 60  |  |
| Db | 1 MALPSRILLKLVLLQSSAVLLHSAVEETDAGLYTCNLLHHYCHLYESLAVLEVTGPP 60  |  |
| Qy | 61 ATPAYWDEGEVLAARGAPALLTCVNRGHVWTDHVEEAQVWHDQPPGVPHDRADR 120   |  |
| Db | 61 ATPAYWDEGEVLAARGAPALLTCVNRGHVWTDHVEEAQVWHDQPPGVPHDRADR 120   |  |
| Qy | 121 LLDLYASGERRAYGFLFDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCG 180   |  |
| Db | 121 LLDLYASGERRAYGFLFDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCG 180   |  |
| Qy | 181 HERRVFLTVAEPAEPHPRGSPGNGSSHGAPDPPTLARGHNVIVIPESRAHFFQ 240   |  |
| Db | 181 HERRVFLTVAEPAEPHPRGSPGNGSSHGAPDPPTLARGHNVIVIPESRAHFFQ 240   |  |
| Qy | 241 LGYVLATLLFILLVTVLLAARRRGYSDQKSGKSGKDVNLAFAVAGDQMLYR 300   |  |
| Db | 241 LGYVLATLLFILLVTVLLAARRRGYSDQKSGKSGKDVNLAFAVAGDQMLYR 300   |  |
| Qy | 301 SEDIQDYKNNILKERAELAHSPAKYIDLKGFRENCK 341  |  |
| Db | 301 SEDIQDYKNNILKERAELAHSPAKYIDLKGFRENCK 341  |  |
| XX | AA99362 standard; Protein; 341 AA.  |  |
| XX | AA99362;  |  |
| XX | 08-AUG-2000 (first entry)   |  |
| XX | Human PRO1293 (UNQ662) amino acid sequence SEQ ID NO:77.  |  |
| XX | Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.   |  |
| XX | Homo sapiens.   |  |
| XX | WO200012708-A2.   |  |

|    |              |               |
|----|--------------|---------------|
| XX | 09-MAR-2000. |               |
| PD | 01-SEP-1999; | 99WO-US20111. |
| XX | 01-SEP-1998; | 98US-0098716. |
| PR | 01-SEP-1998; | 98US-0098749. |
| PR | 01-SEP-1998; | 98US-0098750. |
| PR | 02-SEP-1998; | 98US-0098803. |
| PR | 02-SEP-1998; | 98US-0098821. |
| PR | 02-SEP-1998; | 98US-0098843. |
| PR | 09-SEP-1998; | 98US-0099336. |
| PR | 09-SEP-1998; | 98US-0099396. |
| PR | 09-SEP-1998; | 98US-0099598. |
| PR | 09-SEP-1998; | 98US-0099602. |
| PR | 09-SEP-1998; | 98US-0099642. |
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| PR | 10-SEP-1998; | 98US-0099763. |
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| PR | 10-SEP-1998; | 98US-0099812. |
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| PR | 15-SEP-1998; | 98US-0100385. |
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| PR | 16-SEP-1998; | 98US-0100584. |
| PR | 16-SEP-1998; | 98US-0100627. |
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| PR | 17-SEP-1998; | 98US-0100683. |
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| PR | 17-SEP-1998; | 98US-0100919. |
| PR | 17-SEP-1998; | 98US-0100930. |
| PR | 18-SEP-1998; | 98US-0100848. |
| PR | 18-SEP-1998; | 98US-0100849. |
| PR | 18-SEP-1998; | 98US-0101014. |
| PR | 18-SEP-1998; | 98US-0101068. |
| PR | 18-SEP-1998; | 98US-0101071. |
| PR | 22-SEP-1998; | 98US-0101279. |
| PR | 23-SEP-1998; | 98US-0101471. |
| PR | 23-SEP-1998; | 98US-0101472. |
| PR | 23-SEP-1998; | 98US-0101474. |
| PR | 23-SEP-1998; | 98US-0101475. |
| PR | 23-SEP-1998; | 98US-0101476. |
| PR | 23-SEP-1998; | 98US-0101477. |
| PR | 23-SEP-1998; | 98US-0101479. |
| PR | 24-SEP-1998; | 98US-0101738. |
| PR | 24-SEP-1998; | 98US-0101741. |
| PR | 24-SEP-1998; | 98US-0101743. |
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| PR | 24-SEP-1998; | 98US-0101916. |
| PR | 29-SEP-1998; | 98US-0102207. |
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| PR | 30-SEP-1998; | 98US-0102570. |
| PR | 30-SEP-1998; | 98US-0102571. |
| PR | 01-OCT-1998; | 98US-0102684. |
| PR | 01-OCT-1998; | 98US-0102687. |
| PR | 02-OCT-1998; | 98US-0102965. |
| PR | 06-OCT-1998; | 98US-0103258. |
| PR | 06-OCT-1998; | 98US-0103449. |
| PR | 07-OCT-1998; | 98US-0103314. |
| PR | 07-OCT-1998; | 98US-0103315. |
| PR | 07-OCT-1998; | 98US-0103328. |





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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds  
(without alignments)  
1230.131 Million cell updates/sec

Title: US-10-006-818A-77

Perfect score: 1816

Sequence: 1 MALPSRILLWKLVLQSSAV.....SPLPAKYIDLDKGRKCNCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length DB ID    | Description        |
|------------|--------|-------------|-----------------|--------------------|
| 1          | 1816   | 100.0       | 341 21 AAB24031 | Human PRO1293 prot |
| 2          | 1816   | 100.0       | 341 21 AAY99362 | Human PRO1293 (UNQ |
| 3          | 1816   | 100.0       | 341 22 AAB66111 | Protein of the inv |
| 4          | 1755.5 | 96.7        | 442 22 AAE06578 | Human protein havi |
| 5          | 1755.5 | 96.7        | 442 24 ABB84652 | Human SECP-4 prote |
| 6          | 1706   | 93.9        | 384 21 AAB36107 | Human MTC48. Homo  |
| 7          | 1694.5 | 93.3        | 450 22 AAB92464 | Human protein sequ |
| 8          | 1367.5 | 75.3        | 442 23 ABB72335 | Rat protein isolat |
| 9          | 1362.5 | 75.0        | 442 22 AAB85860 | Murine adipocytes- |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 1300  | 71.6 | 269 | 22 | ABB10350 | Human CDNA SEQ ID  |
| 11 | 1300  | 71.6 | 269 | 23 | ABP66937 | Human polypeptide  |
| 12 | 1006  | 55.4 | 290 | 21 | AAB59011 | Breast and ovarian |
| 13 | 955   | 52.6 | 192 | 22 | AAB10523 | Human CDNA SEQ ID  |
| 14 | 955   | 52.6 | 192 | 22 | AAU18028 | Human immunoglobul |
| 15 | 955   | 52.6 | 192 | 23 | ABP67110 | Human polypeptide  |
| 16 | 840   | 46.3 | 255 | 23 | ABP72366 | Murine protein iso |
| 17 | 826.5 | 45.5 | 260 | 21 | AAB36108 | Mouse MTC48. Mus   |
| 18 | 355   | 19.5 | 218 | 24 | ABB84671 | Human SECP-23 prot |
| 19 | 127   | 7.0  | 447 | 24 | ABR39440 | Human GENSET poly  |
| 20 | 125.5 | 6.9  | 651 | 19 | AAW62782 | Protein encoded by |
| 21 | 125   | 6.9  | 244 | 22 | AAB46060 | Human TF anti-idio |
| 22 | 123   | 6.8  | 650 | 21 | AAW82544 | Human LIR-P3G2 pro |
| 23 | 123   | 6.8  | 650 | 21 | AAB04169 | Leukocyte immunogl |
| 24 | 122   | 6.7  | 253 | 23 | ABP45328 | Human BLYS binding |
| 25 | 122   | 6.7  | 652 | 19 | AAW82545 | Human LIR-18A3 pro |
| 26 | 122   | 6.7  | 652 | 21 | AAB04170 | Leukocyte immunogl |
| 27 | 121   | 6.7  | 254 | 23 | ABP45355 | Human BLYS binding |
| 28 | 120   | 6.6  | 266 | 23 | ABG97835 | Single chain antib |
| 29 | 120   | 6.6  | 266 | 23 | ABG35336 | Thrombopoietin ago |
| 30 | 119.5 | 6.6  | 246 | 21 | AA15126  | Anti-murine CTLA-4 |
| 31 | 119.5 | 6.6  | 249 | 23 | ABP45951 | Human BLYS binding |
| 32 | 119   | 6.6  | 240 | 22 | AAB46058 | Human TF anti-idio |
| 33 | 118.5 | 6.5  | 448 | 19 | AAW82551 | Human LIR-pbm2 pro |
| 34 | 118.5 | 6.5  | 448 | 19 | AAW53463 | Human gp49 HM18 po |
| 35 | 118.5 | 6.5  | 448 | 21 | AAB04176 | Leukocyte immunogl |
| 36 | 118.5 | 6.5  | 469 | 22 | AAW41582 | Human polypeptide  |
| 37 | 117.5 | 6.5  | 472 | 19 | AAW69234 | FCR-IV protein seq |
| 38 | 117   | 6.4  | 239 | 22 | AAB46059 | Human TF anti-idio |
| 39 | 116.5 | 6.4  | 244 | 20 | AA106718 | Antibody 12E10 sin |
| 40 | 116.5 | 6.4  | 328 | 23 | AAO19049 | Cell adhesion mole |
| 41 | 116   | 6.4  | 253 | 23 | ABP45591 | Human BLYS binding |
| 42 | 115.5 | 6.4  | 249 | 23 | ABP45607 | Human BLYS binding |
| 43 | 115.5 | 6.4  | 251 | 23 | ABP45535 | Human BLYS binding |
| 44 | 115.5 | 6.4  | 533 | 22 | AAW93372 | Human polypeptide  |
| 45 | 115.5 | 6.4  | 534 | 22 | AAU00906 | Human B lymphocyte |

ALIGNMENTS

RESULT 1

AAAB24031  
ID AAB24031 standard; Protein; 341 AA.  
XX  
AC AAB24031;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Human PRO1293 protein sequence SEQ ID NO:31.  
XX

Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
identification; tumourigenesis; anticancer; detection.

Homo sapiens.

XX  
FN WO200053750-A1.  
XX

PD 14-SEP-2000

XX  
PF 02-DEC-1999; 99WO-US28551.  
XX

PR 08-MAR-1999; 99WO-US05028.  
XX

PR 01-SEP-1999; 99WO-US20111.  
XX

PR 29-OCT-1999; 99US-0162506.  
XX

PR 30-NOV-1999; 99WO-US28313.  
XX

PR 01-DEC-1999; 99WO-US28634.  
XX

PA (GETH ) GENENTECH INC.

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PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX

DR WPI; 2000-594320/56.

Sequence, A, Comparison

See over